



SEQUENCE LISTING

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<120> Structures of Substrate Binding Pockets of SCF Complexes

<130> 14096.34USU1

<140> US 10/687,732

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<160> 43

<170> PatentIn version 3.2

<210> 1

<211> 8

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(1)

<223> wherein Xaa can be either Ile or Leu

<220>

<221> misc_feature

<222> (2)..(2)

<223> wherein Xaa can be either Ile, Leu or Pro

<220>

<221> MOD_RES

<222> (3)..(3)

<223> PHOSPHORYLATION

<220>

<221> misc_feature

<222> (5)..(5)

<223> wherein Xaa cannot be Lys or Arg

<220>

<221> misc_feature

<222> (6)..(6)

<223> wherein Xaa cannot be Lys or Arg

<220>

<221> misc_feature

<222> (7)..(7)

<223> wherein Xaa cannot be Lys or Arg

<220>

<221> misc_feature

<222> (8)..(8)
<223> wherein Xaa cannot be Lys or Arg

<400> 1

Xaa Xaa Thr Pro Xaa Xaa Xaa Xaa
1 5

<210> 2
<211> 4
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(1)
<223> wherin Xaa may be Ser or Thr

<220>
<221> misc_feature
<222> (3)..(3)
<223> wherin Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (4)..(4)
<223> wherin Xaa can be Lys or Arg

<400> 2

Xaa Pro Xaa Xaa
1

<210> 3
<211> 194
<212> PRT
<213> Saccharomyces cerevisiae

<400> 3

Met Val Thr Ser Asn Val Val Leu Val Ser Gly Glu Gly Glu Arg Phe
1 5 10 15

Thr Val Asp Lys Lys Ile Ala Glu Arg Ser Leu Leu Leu Lys Asn Tyr
20 25 30

Leu Asn Asp Met His Asp Ser Asn Leu Gln Asn Asn Ser Asp Ser Glu
35 40 45

Ser Asp Ser Asp Ser Glu Thr Asn His Lys Ser Lys Asp Asn Asn Asn
50 55 60

Gly Asp Asp Asp Asp Glu Asp Asp Asp Glu Ile Val Met Pro Val Pro

65		70		75		80									
Asn	Val	Arg	Ser	Ser	Val	Leu	Gln	Lys	Val	Ile	Glu	Trp	Ala	Glu	His
			85					90						95	
His	Arg	Asp	Ser	Asn	Phe	Pro	Asp	Glu	Asp	Asp	Asp	Asp	Ser	Arg	Lys
			100					105					110		
Ser	Ala	Pro	Val	Asp	Ser	Trp	Asp	Arg	Glu	Phe	Leu	Lys	Val	Asp	Gln
		115					120					125			
Glu	Met	Leu	Tyr	Glu	Ile	Ile	Leu	Ala	Ala	Asn	Tyr	Leu	Asn	Ile	Lys
	130					135					140				
Pro	Leu	Leu	Asp	Ala	Gly	Cys	Lys	Val	Val	Ala	Glu	Met	Ile	Arg	Gly
145					150					155					160
Arg	Ser	Pro	Glu	Glu	Ile	Arg	Arg	Thr	Phe	Asn	Ile	Val	Asn	Asp	Phe
			165						170					175	
Thr	Pro	Glu	Glu	Glu	Ala	Ala	Ile	Arg	Arg	Glu	Asn	Glu	Trp	Ala	Glu
		180						185					190		
Asp Arg															
<210> 4															
<211> 161															
<212> PRT															
<213> Schizosaccharomyces pombe															
<400> 4															
Met	Ser	Lys	Ile	Lys	Leu	Ile	Ser	Ser	Asp	Asn	Glu	Glu	Phe	Val	Val
1				5					10					15	
Asp	Gln	Leu	Ile	Ala	Glu	Arg	Ser	Met	Leu	Ile	Lys	Asn	Met	Leu	Glu
		20					25						30		
Asp	Val	Gly	Glu	Ile	Asn	Val	Pro	Ile	Pro	Leu	Pro	Asn	Val	Ser	Ser
		35					40					45			
Asn	Val	Leu	Arg	Lys	Val	Leu	Glu	Trp	Cys	Glu	His	His	Lys	Asn	Asp
	50					55					60				
Leu	Tyr	Ser	Gly	Thr	Glu	Glu	Glu	Ser	Asp	Ile	Arg	Leu	Lys	Lys	Ser
65				70						75				80	

Thr Asp Ile Asp Glu Trp Asp Arg Lys Phe Met Ala Val Asp Gln Glu
85 90 95

Met Leu Phe Glu Ile Val Leu Ala Ser Asn Tyr Leu Asp Ile Lys Pro
100 105 110

Leu Leu Asp Thr Gly Cys Lys Thr Val Ala Asn Met Ile Arg Gly Lys
115 120 125

Ser Pro Glu Asp Ile Arg Lys Thr Phe Asn Ile Pro Asn Asp Phe Thr
130 135 140

Pro Glu Glu Glu Glu Gln Ile Arg Lys Glu Asn Glu Trp Ala Glu Asp
145 150 155 160

Arg

<210> 5
<211> 165
<212> PRT
<213> Caenorhabditis elegans

<400> 5

Ala Lys Glu Arg Glu Ile Lys Ile Ser Ser Ser Asp Asn Glu Ile Phe
1 5 10 15

Leu Val Pro Arg Asn Val Ile Arg Leu Ser Asn Thr Ile Asn Thr Leu
20 25 30

Leu Met Asp Leu Gly Leu Asp Asp Glu Glu Gly Thr Asn Ala Glu Pro
35 40 45

Ile Pro Val Gln Asn Val Thr Ala Ser Ile Leu Lys Lys Val Ile Ser
50 55 60

Trp Cys Asn His His His Ser Asp Pro Ile Ser Thr Glu Asp Ser Asp
65 70 75 80

Asn Arg Glu Lys Arg Thr Asp Asp Ile Gly Ser Trp Asp Val Glu Phe
85 90 95

Leu Lys Val Asp Gln Gly Thr Leu Phe Glu Leu Ile Ala Ala Asn Tyr
100 105 110

Leu Asp Ile Lys Gly Leu Leu Asp Val Thr Cys Lys Thr Val Ala Asn
115 120 125

Met Ile Lys Gly Lys Ser Pro Glu Glu Ile Arg Arg Thr Phe Asn Ile
130 135 140

Lys Asn Asp Phe Thr Pro Glu Glu Glu Glu Gln Ile Arg Lys Glu Asn
145 150 155 160

Ala Trp Cys Glu Asp
165

<210> 6
<211> 162
<212> PRT
<213> Drosophila melanogaster

<400> 6

Met Pro Ser Ile Lys Leu Gln Ser Ser Asp Glu Glu Ile Phe Asp Thr
1 5 10 15

Asp Ile Gln Ile Ala Lys Cys Ser Gly Thr Ile Lys Thr Met Leu Glu
20 25 30

Asp Cys Gly Met Glu Asp Asp Glu Asn Ala Ile Val Pro Leu Pro Asn
35 40 45

Val Asn Ser Thr Ile Leu Arg Lys Val Leu Thr Trp Ala His Tyr His
50 55 60

Lys Asp Asp Pro Gln Pro Thr Glu Asp Asp Glu Ser Lys Glu Lys Arg
65 70 75 80

Thr Asp Asp Ile Ile Ser Trp Asp Ala Asp Phe Leu Lys Val Asp Gln
85 90 95

Gly Thr Leu Phe Glu Leu Ile Leu Ala Ala Asn Tyr Leu Asp Ile Lys
100 105 110

Gly Leu Leu Glu Leu Thr Cys Lys Thr Val Ala Asn Met Ile Lys Gly
115 120 125

Lys Thr Pro Glu Glu Ile Arg Lys Thr Phe Asn Ile Lys Lys Asp Phe
130 135 140

Ser Pro Ala Glu Glu Glu Gln Val Arg Lys Glu Asn Glu Trp Cys Glu
 145 150 155 160

Glu Lys

<210> 7
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 7

Met Pro Ser Ile Lys Leu Gln Ser Ser Asp Gly Glu Ile Phe Glu Val
 1 5 10 15

Asp Val Glu Ile Ala Lys Gln Ser Val Thr Ile Lys Thr Met Leu Glu
 20 25 30

Asp Leu Gly Met Asp Asp Glu Gly Asp Asp Asp Pro Val Pro Leu Pro
 35 40 45

Asn Val Asn Ala Ala Ile Leu Lys Lys Val Ile Gln Trp Cys Thr His
 50 55 60

His Lys Asp Asp Pro Pro Pro Pro Glu Asp Asp Glu Asn Lys Glu Lys
 65 70 75 80

Arg Thr Asp Asp Ile Pro Val Trp Asp Gln Glu Phe Leu Lys Val Asp
 85 90 95

Gln Gly Thr Leu Phe Glu Leu Ile Leu Ala Ala Asn Tyr Leu Asp Ile
 100 105 110

Lys Gly Leu Leu Asp Val Thr Cys Lys Thr Val Ala Asn Met Ile Lys
 115 120 125

Gly Lys Thr Pro Glu Glu Ile Arg Lys Thr Phe Asn Ile Lys Asn Asp
 130 135 140

Phe Thr Glu Glu Glu Glu Ala Gln Val Arg Lys Glu Asn Gln Trp Cys
 145 150 155 160

Glu Glu Lys

<210> 8

<211> 475
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 8

Leu	Lys	Arg	Asp	Leu	Ile	Thr	Ser	Leu	Pro	Phe	Glu	Ile	Ser	Leu	Lys	1	5	10	15
Ile	Phe	Asn	Tyr	Leu	Gln	Phe	Glu	Asp	Ile	Ile	Asn	Ser	Leu	Gly	Val	20	25	30	
Ser	Gln	Asn	Trp	Asn	Lys	Ile	Ile	Arg	Lys	Ser	Thr	Ser	Leu	Trp	Lys	35	40	45	
Lys	Leu	Leu	Ile	Ser	Glu	Asn	Phe	Val	Ser	Pro	Lys	Gly	Phe	Asn	Ser	50	55	60	
Leu	Asn	Leu	Lys	Leu	Ser	Gln	Lys	Tyr	Pro	Lys	Leu	Ser	Gln	Gln	Asp	65	70	75	80
Arg	Leu	Arg	Leu	Ser	Phe	Leu	Glu	Asn	Ile	Phe	Ile	Leu	Lys	Asn	Trp	85	90	95	
Tyr	Asn	Pro	Lys	Phe	Val	Pro	Gln	Arg	Thr	Thr	Leu	Arg	Gly	His	Met	100	105	110	
Thr	Ser	Val	Ile	Thr	Cys	Leu	Gln	Phe	Glu	Asp	Asn	Tyr	Val	Ile	Thr	115	120	125	
Gly	Ala	Asp	Asp	Lys	Met	Ile	Arg	Val	Tyr	Asp	Ser	Ile	Asn	Lys	Lys	130	135	140	
Phe	Leu	Leu	Gln	Leu	Ser	Gly	His	Asp	Gly	Gly	Val	Trp	Ala	Leu	Lys	145	150	155	160
Tyr	Ala	His	Gly	Gly	Ile	Leu	Val	Ser	Gly	Ser	Thr	Asp	Arg	Thr	Val	165	170	175	
Arg	Val	Trp	Asp	Ile	Lys	Lys	Gly	Cys	Cys	Thr	His	Val	Phe	Lys	Gly	180	185	190	
His	Asn	Ser	Thr	Val	Arg	Cys	Leu	Asp	Ile	Val	Glu	Tyr	Lys	Asn	Ile	195	200	205	
Lys	Tyr	Ile	Val	Thr	Gly	Ser	Arg	Asp	Asn	Thr	Leu	His	Val	Trp	Lys	210	215	220	

Leu Pro Lys Glu Ser Ser Val Pro Asp His Gly Glu Glu His Asp Tyr
 225 230 235 240

Pro Leu Val Phe His Thr Pro Glu Glu Asn Pro Tyr Phe Val Gly Val
 245 250 255

Leu Arg Gly His Met Ala Ser Val Arg Thr Val Ser Gly His Gly Asn
 260 265 270

Ile Val Val Ser Gly Ser Tyr Asp Asn Thr Leu Ile Val Trp Asp Val
 275 280 285

Ala Gln Met Lys Cys Leu Tyr Ile Leu Ser Gly His Thr Asp Arg Ile
 290 295 300

Tyr Ser Thr Ile Tyr Asp His Glu Arg Lys Arg Cys Ile Ser Ala Ser
 305 310 315 320

Met Asp Thr Thr Ile Arg Ile Trp Asp Leu Glu Asn Ile Trp Asn Asn
 325 330 335

Gly Glu Cys Ser Tyr Ala Thr Asn Ser Ala Ser Pro Cys Ala Lys Ile
 340 345 350

Leu Gly Ala Met Tyr Thr Leu Gln Gly His Thr Ala Leu Val Gly Leu
 355 360 365

Leu Arg Leu Ser Asp Lys Phe Leu Val Ser Ala Ala Ala Asp Gly Ser
 370 375 380

Ile Arg Gly Trp Asp Ala Asn Asp Tyr Ser Arg Lys Phe Ser Tyr His
 385 390 395 400

His Thr Asn Leu Ser Ala Ile Thr Thr Phe Tyr Val Ser Asp Asn Ile
 405 410 415

Leu Val Ser Gly Ser Glu Asn Gln Phe Asn Ile Tyr Asn Leu Arg Ser
 420 425 430

Gly Lys Leu Val His Ala Asn Ile Leu Lys Asp Ala Asp Gln Ile Trp
 435 440 445

Ser Val Asn Phe Lys Gly Lys Thr Leu Val Ala Ala Val Glu Lys Asp
 450 455 460

Gly Gln Ser Phe Leu Glu Ile Leu Asp Phe Ser
 465 470 475

<210> 9
 <211> 475
 <212> PRT
 <213> Schizosaccharomyces pombe

<400> 9

Phe Gln Lys Asn Phe Leu Thr Gly Phe Pro Ala Glu Ile Thr Asn Leu
 1 5 10 15

Val Leu Thr His Leu Asp Ala Pro Ser Leu Cys Ala Val Ser Gln Val
 20 25 30

Ser His His Trp Tyr Lys Leu Val Ser Ser Asn Glu Glu Leu Trp Lys
 35 40 45

Ser Leu Phe Leu Lys Asp Gly Phe Phe Trp Asp Ser Ile Asp Ser Lys
 50 55 60

Ile Arg Thr Met Cys Leu Glu Gln Ser Leu Ser Ala Cys Ala Ile Met
 65 70 75 80

Lys Arg Val Tyr Phe Arg His Phe Asn Leu Arg Glu Arg Trp Leu His
 85 90 95

Ala Pro Glu Lys Ile Lys Arg Cys Ser Phe Pro Ile His Gly Val Arg
 100 105 110

Leu Ile Thr Lys Leu Gln Phe Asp Asp Asp Lys Ile Ile Val Ser Thr
 115 120 125

Cys Ser Pro Arg Ile Asn Ile Tyr Asp Thr Lys Thr Gly Val Leu Ile
 130 135 140

Arg Ser Leu Glu Glu His Glu Gly Asp Val Trp Thr Phe Glu Tyr Val
 145 150 155 160

Gly Asp Thr Leu Val Thr Gly Ser Thr Asp Arg Thr Val Arg Val Trp
 165 170 175

Asp Leu Arg Thr Gly Glu Cys Lys Gln Val Phe Tyr Gly His Thr Ser
 180 185 190

Thr Ile Arg Cys Ile Lys Ile Val Gln Gly Asn Gln Ser Thr Thr Asp
 195 200 205

Thr Asp Asp Val Glu Lys Glu Asn Arg Pro Ala Ser Asn Asp Ala Asn
 210 215 220

Ser Met Pro Pro Tyr Ile Ile Ser Ser Ser Arg Asp Cys Thr Ile Arg
 225 230 235 240

Leu Trp Ser Leu Pro Cys Leu Asp Asp Pro Pro Phe Val Asn Val Asn
 245 250 255

Glu Asn Pro Asp Gln Asn Asn Asp Phe Thr Ser Ala Thr Thr Asn Pro
 260 265 270

Phe Tyr Ile Arg Thr Leu Arg Gly His Thr Asp Ser Val Arg Glu Val
 275 280 285

Ala Cys Leu Gly Asp Leu Ile Val Ser Ala Ser Tyr Asp Gly Thr Leu
 290 295 300

Arg Val Trp Lys Ala Ser Thr Gly Val Cys Leu His Val Leu Arg Gly
 305 310 315 320

His Val Gly Arg Val Tyr Ser Val Thr Ile Asn Pro Ser Arg Gln Gln
 325 330 335

Cys Ile Ser Ala Gly Thr Asp Ala Lys Ile Arg Ile Trp Asn Leu Glu
 340 345 350

Ser Gly Glu Leu Leu Gln Thr Leu His Gly His Ser Asn Leu Val Ser
 355 360 365

Gln Val Thr Phe Asn Gln Asn Ile Leu Val Ser Ala Ser Ala Pro Pro
 370 375 380

Asp Thr Ser Leu Arg Val Trp Asp Leu Asn Thr Gly Ser Cys Arg Asp
 385 390 395 400

Ile Leu Lys Cys Pro Leu Gly His Ile Phe Phe Gln His Asp Glu Ser
 405 410 415

Lys Val Val Ser Gly Ser His Ser Thr Leu Gln Leu Trp Asp Ile Arg
 420 425 430

Ser Gly Lys Leu Val Arg Asp Leu Leu Thr Asp Leu Asp Ile Ile Trp
435 440 445

Gln Val Ala Tyr Asn Glu Asn Val Cys Val Ala Ala Val Leu Arg Asn
450 455 460

Asn Arg Phe Trp Ile Glu Val Leu Glu Phe Gly
465 470 475

<210> 10
<211> 465
<212> PRT
<213> Caenorhabditis elegans

<400> 10

Phe Gln Arg Asp Phe Leu Ser Cys Leu Pro Val Glu Leu Gly Met Lys
1 5 10 15

Ile Leu His Asn Leu Thr Gly Tyr Asp Leu Leu Lys Val Ala Gln Val
20 25 30

Ser Lys Asn Trp Lys Leu Ile Ser Glu Ile Asp Lys Ile Trp Lys Ser
35 40 45

Leu Gly Val Glu Glu Phe Lys His His Pro Asp Pro Thr Asp Arg Val
50 55 60

Thr Gly Ala Trp Gln Gly Thr Ala Ile Ala Ala Gly Val Thr Ile Pro
65 70 75 80

Asp His Ile Gln Pro Cys Asp Leu Asn Val His Arg Phe Leu Lys Leu
85 90 95

Gln Lys Phe Gly Asp Ile Phe Glu Arg Ala Ala Asp Lys Ser Arg Tyr
100 105 110

Leu Arg Ala Asp Lys Ile Glu Lys Asn Trp Asn Ala Asn Pro Ile Met
115 120 125

Gly Ser Ala Val Leu Arg Gly His Glu Asp His Val Ile Thr Cys Met
130 135 140

Gln Ile His Asp Asp Val Leu Val Thr Gly Ser Asp Asp Asn Thr Leu
145 150 155 160

Lys Val Trp Cys Ile Asp Lys Gly Glu Val Met Tyr Thr Leu Val Gly
 165 170 175

His Thr Gly Gly Val Trp Thr Ser Gln Ile Ser Gln Cys Gly Arg Tyr
 180 185 190

Ile Val Ser Gly Ser Thr Asp Arg Thr Val Lys Val Trp Ser Thr Val
 195 200 205

Asp Gly Ser Leu Leu His Thr Leu Gln Gly His Thr Ser Thr Val Arg
 210 215 220

Cys Met Ala Met Ala Gly Ser Ile Leu Val Thr Gly Ser Arg Asp Thr
 225 230 235 240

Thr Leu Arg Val Trp Asp Val Glu Ser Gly Arg His Leu Ala Thr Leu
 245 250 255

His Gly His His Ala Ala Val Arg Cys Val Gln Phe Asp Gly Thr Thr
 260 265 270

Val Val Ser Gly Gly Tyr Asp Phe Thr Val Lys Ile Trp Asn Ala His
 275 280 285

Thr Gly Arg Cys Ile Arg Thr Leu Thr Gly His Asn Asn Arg Val Tyr
 290 295 300

Ser Leu Leu Phe Glu Ser Glu Arg Ser Ile Val Cys Ser Gly Ser Leu
 305 310 315 320

Asp Thr Ser Ile Arg Val Trp Asp Phe Thr Arg Pro Glu Gly Gln Glu
 325 330 335

Cys Val Ala Leu Leu Gln Gly His Thr Ser Leu Thr Ser Gly Met Gln
 340 345 350

Leu Arg Gly Asn Ile Leu Val Ser Cys Asn Ala Asp Ser His Val Arg
 355 360 365

Val Trp Asp Ile His Glu Gly Thr Cys Val His Met Leu Ser Gly His
 370 375 380

Arg Ser Ala Ile Thr Ser Leu Gln Trp Phe Gly Arg Asn Met Val Ala
 385 390 395 400

Thr Ser Ser Asp Asp Gly Thr Val Lys Leu Trp Asp Ile Glu Arg Gly
 405 410 415

Ala Leu Ile Arg Asp Leu Val Thr Leu Asp Ser Gly Gly Asn Gly Gly
 420 425 430

Cys Ile Trp Arg Leu Cys Ser Thr Ser Thr Met Leu Ala Cys Ala Val
 435 440 445

Gly Ser Arg Asn Asn Thr Glu Glu Thr Lys Val Ile Leu Leu Asp Phe
 450 455 460

Asp
 465

<210> 11
 <211> 431
 <212> PRT
 <213> Drosophila melanogaster

<400> 11

Phe Gln Arg Asp Phe Ile Ser Leu Leu Pro Arg Glu Leu Ala Leu Phe
 1 5 10 15

Val Leu Ser Tyr Leu Glu Pro Lys Asp Leu Leu Arg Ala Ala Gln Thr
 20 25 30

Cys Arg Ser Trp Arg Phe Leu Cys Asp Asp Asn Leu Leu Trp Lys Glu
 35 40 45

Lys Cys Arg Lys Ala Gln Ile Leu Ala Glu Pro Arg Ser Asp Arg Pro
 50 55 60

Lys Arg Gly Arg Asp Gly Asn Met Pro Pro Ile Ala Ser Pro Trp Lys
 65 70 75 80

Ala Ala Tyr Met Arg Gln His Ile Ile Glu Met Asn Trp Arg Ser Arg
 85 90 95

Pro Val Arg Lys Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile
 100 105 110

Thr Cys Leu Gln Phe Ser Gly Asn Arg Ile Val Ser Gly Ser Asp Asp
 115 120 125

Asn Thr Leu Lys Val Trp Ser Ala Val Asn Gly Lys Cys Leu Arg Thr

130	135	140
Leu Val Gly His Thr Gly Gly Val Trp Ser Ser Gln Met Ser Gly Asn 145 150 155 160		
Ile Ile Ile Ser Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asp Met 165 170 175		
Asp Ser Gly Ala Cys Val His Thr Leu Gln Gly His Thr Ser Thr Val 180 185 190		
Arg Cys Met His Leu His Gly Ser Lys Val Val Ser Gly Ser Arg Asp 195 200 205		
Ala Thr Leu Arg Val Trp Asp Ile Glu Gln Gly Ser Cys Leu His Val 210 215 220		
Leu Val Gly His Leu Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Lys 225 230 235 240		
Leu Ile Val Ser Gly Ala Tyr Asp Tyr Met Val Lys Ile Trp His Pro 245 250 255		
Glu Arg Gln Glu Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val 260 265 270		
Tyr Ser Leu Gln Phe Asp Gly Leu His Val Val Ser Gly Ser Leu Asp 275 280 285		
Thr Ser Ile Arg Val Trp Asp Val Glu Thr Gly Asn Cys Lys His Thr 290 295 300		
Leu Met Gly His Gln Ser Leu Thr Ser Gly Met Glu Leu Arg Gln Asn 305 310 315 320		
Ile Leu Val Ser Gly Asn Ala Asp Ser Thr Val Lys Val Trp Asp Ile 325 330 335		
Thr Thr Gly Gln Cys Leu Gln Thr Leu Ser Gly Pro Asn Lys His His 340 345 350		
Ser Ala Val Thr Cys Leu Gln Phe Asn Ser Arg Phe Val Val Thr Ser 355 360 365		
Ser Asp Asp Gly Thr Val Lys Leu Trp Asp Val Lys Thr Gly Asp Phe		

370

375

380

Ile Arg Asn Leu Val Ala Leu Asp Ser Gly Gly Ser Gly Gly Val Val
 385 390 395 400

Trp Arg Ile Arg Ala Asn Asp Thr Lys Leu Ile Cys Ala Val Gly Ser
 405 410 415

Arg Asn Gly Thr Glu Glu Thr Lys Leu Met Val Leu Asp Phe Asp
 420 425 430

<210> 12

<211> 428

<212> PRT

<213> Homo sapiens

<400> 12

Phe Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu Ala Leu Tyr
 1 5 10 15

Val Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala Ala Gln Thr
 20 25 30

Cys Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu Trp Arg Glu
 35 40 45

Lys Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile Lys Arg Arg
 50 55 60

Lys Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys Ser Ala Tyr
 65 70 75 80

Ile Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly Glu Leu Lys
 85 90 95

Ser Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile Thr Cys Leu
 100 105 110

Gln Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asp Asn Thr Leu
 115 120 125

Lys Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr Leu Val Gly
 130 135 140

His Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn Ile Ile Ile
 145 150 155 160

Ser Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala Glu Thr Gly
 165 170 175

Glu Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val Arg Cys Met
 180 185 190

His Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp Ala Thr Leu
 195 200 205

Arg Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val Leu Met Gly
 210 215 220

His Val Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Arg Arg Val Val
 225 230 235 240

Ser Gly Ala Tyr Asp Phe Met Val Lys Val Trp Asp Pro Glu Thr Glu
 245 250 255

Thr Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val Tyr Ser Leu
 260 265 270

Gln Phe Asp Gly Ile His Val Val Ser Gly Ser Leu Asp Thr Ser Ile
 275 280 285

Arg Val Trp Asp Val Glu Thr Gly Asn Cys Ile His Thr Leu Thr Gly
 290 295 300

His Gln Ser Leu Thr Ser Gly Met Glu Leu Lys Asp Asn Ile Leu Val
 305 310 315 320

Ser Gly Asn Ala Asp Ser Thr Val Lys Ile Trp Asp Ile Lys Thr Gly
 325 330 335

Gln Cys Leu Gln Thr Leu Gln Gly Pro Asn Lys His Gln Ser Ala Val
 340 345 350

Thr Cys Leu Gln Phe Asn Lys Asn Phe Val Ile Thr Ser Ser Asp Asp
 355 360 365

Gly Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile Arg Asn
 370 375 380

Leu Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val Trp Arg Ile
 385 390 395 400

Arg Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser Arg Asn Gly
405 410 415

Thr Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp
420 425

<210> 13
<211> 424
<212> PRT
<213> Caenorhabditis elegans

<400> 13

Leu Gln Arg Asp Phe Ile Ser Asn Leu Pro Ala His Leu Val Glu Leu
1 5 10 15

Ile Leu Phe Asn Val Asn Ser Asp Ser Leu Lys Ser Cys Glu Glu Val
20 25 30

Ser Thr Ser Trp Arg Cys Ala Leu Ala Arg Gly Gln His Trp Lys Lys
35 40 45

Leu Ile Glu Lys Asn Val Arg Ser Asp Ser Leu Trp Trp Gly Leu Ser
50 55 60

Glu Lys Arg Gln Trp Asp Lys Phe Leu Asn Ile Ser Arg Asp Met Ser
65 70 75 80

Val Arg Arg Ile Cys Glu Lys Phe Asn Tyr Asp Val Asn Ile Lys Arg
85 90 95

Asp Lys Leu Asp Gln Leu Ile Leu Met His Val Phe Tyr Ser Lys Leu
100 105 110

Tyr Pro Lys Ile Ile Arg Asp Ile His Asn Ile Asp Asn Asn Trp Lys
115 120 125

Arg Gly Asn Tyr Lys Met Thr Arg Ile Asn Cys Gln Ser Glu Asn Ser
130 135 140

Lys Gly Val Tyr Cys Leu Gln Tyr Asp Asp Lys Ile Val Ser Gly
145 150 155 160

Leu Arg Asp Asn Thr Ile Lys Ile Trp Asp Arg Lys Asp Tyr Ser Cys
165 170 175

Ser Arg Ile Leu Ser Gly His Thr Gly Ser Val Leu Cys Leu Gln Tyr
 180 185 190

Asp Asn Arg Val Ile Ile Ser Gly Ser Ser Asp Ala Thr Val Arg Val
 195 200 205

Trp Asp Val Glu Thr Gly Glu Cys Ile Lys Thr Leu Ile His His Cys
 210 215 220

Glu Ala Val Leu His Leu Arg Phe Ala Asn Gly Ile Met Val Thr Cys
 225 230 235 240

Ser Lys Asp Arg Ser Ile Ala Val Trp Asp Met Val Ser Pro Arg Asp
 245 250 255

Ile Thr Ile Arg Arg Val Leu Val Gly His Arg Ala Ala Val Asn Val
 260 265 270

Val Asp Phe Asp Asp Arg Tyr Ile Val Ser Ala Ser Gly Asp Arg Thr
 275 280 285

Ile Lys Val Trp Ser Met Asp Thr Leu Glu Phe Val Arg Thr Leu Ala
 290 295 300

Gly His Arg Arg Gly Ile Ala Cys Leu Gln Tyr Arg Gly Arg Leu Val
 305 310 315 320

Val Ser Gly Ser Ser Asp Asn Thr Ile Arg Leu Trp Asp Ile His Ser
 325 330 335

Gly Val Cys Leu Arg Val Leu Glu Gly His Glu Glu Leu Val Arg Cys
 340 345 350

Ile Arg Phe Asp Glu Lys Arg Ile Val Ser Gly Ala Tyr Asp Gly Lys
 355 360 365

Ile Lys Val Trp Asp Leu Gln Ala Ala Leu Asp Pro Arg Ala Leu Ser
 370 375 380

Ser Glu Ile Cys Leu Cys Ser Leu Val Gln His Thr Gly Arg Val Phe
 385 390 395 400

Arg Leu Gln Phe Asp Asp Phe Gln Ile Val Ser Ser Ser His Asp Asp
 405 410 415

Thr Ile Leu Ile Trp Asp Phe Leu
420

<210> 14
<211> 407
<212> PRT
<213> Drosophila melanogaster

<400> 14

Leu Gln Arg Asp Phe Ile Thr Leu Leu Pro Ile Lys Gly Leu Asp His
1 5 10 15

Ile Ala Glu Asn Ile Leu Ser Tyr Leu Asp Ala Glu Ser Leu Lys Ser
20 25 30

Ser Glu Leu Val Cys Lys Glu Trp Leu Arg Val Ile Ser Glu Gly Met
35 40 45

Leu Trp Lys Lys Leu Ile Glu Arg Lys Val Arg Thr Asp Ser Leu Trp
50 55 60

Arg Gly Leu Ala Glu Arg Arg Asn Trp Met Gln Tyr Leu Phe Lys Pro
65 70 75 80

Arg Pro Gly Gln Thr Gln Arg Pro His Ser Phe His Arg Glu Leu Phe
85 90 95

Pro Lys Ile Met Asn Asp Ile Asp Ser Ile Glu Asn Asn Trp Arg Thr
100 105 110

Gly Arg His Met Leu Arg Arg Ile Asn Cys Arg Ser Glu Asn Ser Lys
115 120 125

Gly Val Tyr Cys Leu Gln Tyr Asp Asp Gly Lys Ile Val Ser Gly Leu
130 135 140

Arg Asp Asn Thr Ile Lys Ile Trp Asp Arg Thr Asp Leu Gln Cys Val
145 150 155 160

Lys Thr Leu Met Gly His Thr Gly Ser Val Leu Cys Leu Gln Tyr Asp
165 170 175

Asp Lys Val Ile Ile Ser Gly Ser Ser Asp Ser Thr Val Arg Val Trp
180 185 190

Asp Val Asn Thr Gly Glu Met Val Asn Thr Leu Ile His His Cys Glu
195 200 205

Ala Val Leu His Leu Arg Phe Asn Asn Gly Met Met Val Thr Cys Ser
210 215 220

Lys Asp Arg Ser Ile Ala Val Trp Asp Met Thr Ser Pro Ser Glu Ile
225 230 235 240

Thr Leu Arg Arg Val Leu Val Gly His Arg Ala Ala Val Asn Val Val
245 250 255

Asp Phe Asp Glu Lys Tyr Ile Val Ser Ala Ser Gly Asp Arg Thr Ile
260 265 270

Lys Val Trp Ser Thr Ser Ser Cys Glu Phe Val Arg Thr Leu Asn Gly
275 280 285

His Lys Arg Gly Ile Ala Cys Leu Gln Tyr Arg Asp Arg Leu Val Val
290 295 300

Ser Gly Ser Ser Asp Asn Ser Ile Arg Leu Trp Asp Ile Glu Cys Gly
305 310 315 320

Ala Cys Leu Arg Val Leu Glu Gly His Glu Glu Leu Val Arg Cys Ile
325 330 335

Arg Phe Asp Thr Lys Arg Ile Val Ser Gly Ala Tyr Asp Gly Lys Ile
340 345 350

Lys Val Trp Asp Leu Val Ala Ala Leu Asp Pro Arg Ala Ala Ser Asn
355 360 365

Thr Leu Cys Leu Asn Thr Leu Val Glu His Thr Gly Arg Val Phe Arg
370 375 380

Leu Gln Phe Asp Glu Phe Gln Ile Val Ser Ser Ser His Asp Asp Thr
385 390 395 400

Ile Leu Ile Trp Asp Phe Leu
405

<210> 15
<211> 408
<212> PRT
<213> Homo sapiens

<400> 15

Leu Gln Arg Asp Phe Ile Thr Ala Leu Pro Ala Arg Gly Leu Asp His
1 5 10 15

Ile Ala Glu Asn Ile Leu Ser Tyr Leu Asp Ala Lys Ser Leu Cys Ala
20 25 30

Ala Glu Leu Val Cys Lys Glu Trp Tyr Arg Val Thr Ser Asp Gly Met
35 40 45

Leu Trp Lys Lys Leu Ile Glu Arg Met Val Arg Thr Asp Ser Leu Trp
50 55 60

Arg Gly Leu Ala Glu Arg Arg Gly Trp Gly Gln Tyr Leu Phe Lys Asn
65 70 75 80

Lys Pro Pro Asp Gly Asn Ala Pro Pro Asn Ser Phe Tyr Arg Ala Leu
85 90 95

Tyr Pro Lys Ile Ile Gln Asp Ile Glu Thr Ile Glu Ser Asn Trp Arg
100 105 110

Cys Gly Arg His Ser Leu Gln Arg Ile His Cys Arg Ser Glu Thr Ser
115 120 125

Lys Gly Val Tyr Cys Leu Gln Tyr Asp Asp Gln Lys Ile Val Ser Gly
130 135 140

Leu Arg Asp Asn Thr Ile Lys Ile Trp Asp Lys Asn Thr Leu Glu Cys
145 150 155 160

Lys Arg Ile Leu Thr Gly His Thr Gly Ser Val Leu Cys Leu Gln Tyr
165 170 175

Asp Glu Arg Val Ile Ile Thr Gly Ser Ser Asp Ser Thr Val Arg Val
180 185 190

Trp Asp Val Asn Thr Gly Glu Met Leu Asn Thr Leu Ile His His Cys
195 200 205

Glu Ala Val Leu His Leu Arg Phe Asn Asn Gly Met Met Val Thr Cys
210 215 220

Ser Lys Asp Arg Ser Ile Ala Val Trp Asp Met Ala Ser Pro Thr Asp
21

225						230						235						240
Ile	Thr	Leu	Arg	Arg	Val	Leu	Val	Gly	His	Arg	Ala	Ala	Val	Asn	Val			
				245					250					255				
Val	Asp	Phe	Asp	Asp	Lys	Tyr	Ile	Val	Ser	Ala	Ser	Gly	Asp	Arg	Thr			
				260					265					270				
Ile	Lys	Val	Trp	Asn	Thr	Ser	Thr	Cys	Glu	Phe	Val	Arg	Thr	Leu	Asn			
				275					280					285				
Gly	His	Lys	Arg	Gly	Ile	Ala	Cys	Leu	Gln	Tyr	Arg	Asp	Arg	Leu	Val			
				290					295					300				
Val	Ser	Gly	Ser	Ser	Asp	Asn	Thr	Ile	Arg	Leu	Trp	Asp	Ile	Glu	Cys			
305					310					315					320			
Gly	Ala	Cys	Leu	Arg	Val	Leu	Glu	Gly	His	Glu	Glu	Leu	Val	Arg	Cys			
				325					330					335				
Ile	Arg	Phe	Asp	Asn	Lys	Arg	Ile	Val	Ser	Gly	Ala	Tyr	Asp	Gly	Lys			
				340					345					350				
Ile	Lys	Val	Trp	Asp	Leu	Val	Ala	Ala	Leu	Asp	Pro	Arg	Ala	Pro	Ala			
				355					360					365				
Gly	Thr	Leu	Cys	Leu	Arg	Thr	Leu	Val	Glu	His	Ser	Gly	Arg	Val	Phe			
				370					375					380				
Arg	Leu	Gln	Phe	Asp	Glu	Phe	Gln	Ile	Val	Ser	Ser	Ser	His	Asp	Asp			
385					390					395					400			
Thr	Ile	Leu	Ile	Trp	Asp	Phe	Leu											
				405														

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<210> 16
<211> 459
<212> PRT
<213> Saccharomyces cerevisiae
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<400> 16

Ile Lys Ile Asp Phe Ile Ser Ile Leu Pro Gln Glu Leu Ser Leu Lys
1 5 10 15

Ile Leu Ser Tyr Leu Asp Cys Gln Ser Leu Cys Asn Ala Thr Arg Val
20 25 30

Cys Arg Lys Trp Gln Lys Leu Ala Asp Asp Asp Arg Val Trp Tyr His
 35 40 45
 Met Cys Glu Gln His Ile Asp Arg Lys Cys Pro Asn Cys Gly Trp Gly
 50 55 60
 Leu Pro Leu Leu His Met Lys Arg Ala Arg Ile Gln Gln Asn Ser Thr
 65 70 75 80
 Gly Ser Ser Ser Asn Ala Asp Ile Gln Thr Gln Thr Thr Arg Pro Trp
 85 90 95
 Lys Val Ile Tyr Arg Glu Arg Phe Lys Val Glu Ser Asn Trp Arg Lys
 100 105 110
 Gly His Cys Arg Ile Gln Glu Phe Lys Gly His Met Asp Gly Val Leu
 115 120 125
 Thr Leu Gln Phe Asn Tyr Arg Leu Leu Phe Thr Gly Ser Tyr Asp Ser
 130 135 140
 Thr Ile Gly Ile Trp Asp Leu Phe Thr Gly Lys Leu Ile Arg Arg Leu
 145 150 155 160
 Ser Gly His Ser Asp Gly Val Lys Thr Leu Tyr Phe Asp Asp Arg Lys
 165 170 175
 Leu Ile Thr Gly Ser Leu Asp Lys Thr Ile Arg Val Trp Asn Tyr Ile
 180 185 190
 Thr Gly Glu Cys Ile Ser Thr Tyr Arg Gly His Ser Asp Ser Val Leu
 195 200 205
 Ser Val Asp Ser Tyr Gln Lys Val Ile Val Ser Gly Ser Ala Asp Lys
 210 215 220
 Thr Val Lys Val Trp His Val Glu Ser Arg Thr Cys Tyr Thr Leu Arg
 225 230 235 240
 Gly His Thr Glu Trp Val Asn Cys Val Lys Leu His Pro Lys Ser Phe
 245 250 255
 Ser Cys Phe Ser Cys Ser Asp Asp Thr Thr Ile Arg Met Trp Asp Ile
 260 265 270

Arg Thr Asn Ser Cys Leu Lys Val Phe Arg Gly His Val Gly Gln Val
 275 280 285

Gln Lys Ile Ile Pro Leu Thr Ile Lys Asp Val Glu Asn Leu Ala Thr
 290 295 300

Asp Asn Thr Ser Asp Gly Ser Ser Pro Gln Asp Asp Pro Thr Met Thr
 305 310 315 320

Asp Gly Ala Asp Glu Ser Asp Thr Pro Ser Asn Glu Gln Glu Thr Val
 325 330 335

Leu Asp Glu Asn Ile Pro Tyr Pro Thr His Leu Leu Ser Cys Gly Leu
 340 345 350

Asp Asn Thr Ile Lys Leu Trp Asp Val Lys Thr Gly Lys Cys Ile Arg
 355 360 365

Thr Gln Phe Gly His Val Glu Gly Val Trp Asp Ile Ala Ala Asp Asn
 370 375 380

Phe Arg Ile Ile Ser Gly Ser His Asp Gly Ser Ile Lys Val Trp Asp
 385 390 395 400

Leu Gln Ser Gly Lys Cys Met His Thr Phe Asn Gly Arg Arg Leu Gln
 405 410 415

Arg Glu Thr Gln His Thr Gln Thr Gln Ser Leu Gly Asp Lys Val Ala
 420 425 430

Pro Ile Ala Cys Val Cys Ile Gly Asp Ser Glu Cys Phe Ser Gly Asp
 435 440 445

Glu Phe Gly Cys Val Lys Met Tyr Lys Phe Asp
 450 455

<210> 17
 <211> 640
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<300>
 <308> Genbank/P39014
 <309> 1995-02-01
 <313> (1) .. (640)

<400> 17

Met Arg Arg Glu Arg Gln Arg Met Met Ser Phe Glu Asp Lys Asp Lys
1 5 10 15

Asp Asp Leu Asp Asn Ser Asn Ser Asn Asn Ser Ser Glu Met Thr Asp
20 25 30

Thr Ala Met Met Pro Pro Leu Lys Arg Leu Leu Ile Thr Gly Ser Ser
35 40 45

Asp Asp Leu Ala Gln Gly Ser Ser Gly Lys Lys Lys Met Thr Met Ala
50 55 60

Thr Arg Ser Pro Ser Ser Ser Pro Asp Leu Ala Thr Asn Asp Ser Gly
65 70 75 80

Thr Arg Val Gln Pro Leu Pro Glu Tyr Asn Phe Thr Lys Phe Cys Tyr
85 90 95

Arg His Asn Pro Asp Ile Gln Phe Ser Pro Thr His Thr Ala Cys Tyr
100 105 110

Lys Gln Asp Leu Lys Arg Thr Gln Glu Ile Asn Ala Asn Ile Ala Lys
115 120 125

Leu Pro Leu Gln Glu Gln Ser Asp Ile His His Ile Ile Ser Lys Tyr
130 135 140

Ser Asn Ser Asn Asp Lys Ile Arg Lys Leu Ile Leu Asp Gly Ile Leu
145 150 155 160

Ser Thr Ser Cys Phe Pro Gln Leu Ser Tyr Ile Ser Ser Leu Val Thr
165 170 175

His Met Ile Lys Ile Asp Phe Ile Ser Ile Leu Pro Gln Glu Leu Ser
180 185 190

Leu Lys Ile Leu Ser Tyr Leu Asp Cys Gln Ser Leu Cys Asn Ala Thr
195 200 205

Arg Val Cys Arg Lys Trp Gln Lys Leu Ala Asp Asp Asp Arg Val Trp
210 215 220

Tyr His Met Cys Glu Gln His Ile Asp Arg Lys Cys Pro Asn Cys Gly
225 230 235 240

Trp Gly Leu Pro Leu Leu His Met Lys Arg Ala Arg Ile Gln Gln Asn
 245 250 255

Ser Thr Gly Ser Ser Ser Asn Ala Asp Ile Gln Thr Gln Thr Thr Arg
 260 265 270

Pro Trp Lys Val Ile Tyr Arg Glu Arg Phe Lys Val Glu Ser Asn Trp
 275 280 285

Arg Lys Gly His Cys Arg Ile Gln Glu Phe Lys Gly His Met Asp Gly
 290 295 300

Val Leu Thr Leu Gln Phe Asn Tyr Arg Leu Leu Phe Thr Gly Ser Tyr
 305 310 315 320

Asp Ser Thr Ile Gly Ile Trp Asp Leu Phe Thr Gly Lys Leu Ile Arg
 325 330 335

Arg Leu Ser Gly His Ser Asp Gly Val Lys Thr Leu Tyr Phe Asp Asp
 340 345 350

Arg Lys Leu Ile Thr Gly Ser Leu Asp Lys Thr Ile Arg Val Trp Asn
 355 360 365

Tyr Ile Thr Gly Glu Cys Ile Ser Thr Tyr Arg Gly His Ser Asp Ser
 370 375 380

Val Leu Ser Val Asp Ser Tyr Gln Lys Val Ile Val Ser Gly Ser Ala
 385 390 395 400

Asp Lys Thr Val Lys Val Trp His Val Glu Ser Arg Thr Cys Tyr Thr
 405 410 415

Leu Arg Gly His Thr Glu Trp Val Asn Cys Val Lys Leu His Pro Lys
 420 425 430

Ser Phe Ser Cys Phe Ser Cys Ser Asp Asp Thr Thr Ile Arg Met Trp
 435 440 445

Asp Ile Arg Thr Asn Ser Cys Leu Lys Val Phe Arg Gly His Val Gly
 450 455 460

Gln Val Gln Lys Ile Ile Pro Leu Thr Ile Lys Asp Val Glu Asn Leu
 465 470 475 480

Ala Thr Asp Asn Thr Ser Asp Gly Ser Ser Pro Gln Asp Asp Pro Thr
485 490 495

Met Thr Asp Gly Ala Asp Glu Ser Asp Thr Pro Ser Asn Glu Gln Glu
500 505 510

Thr Val Leu Asp Glu Asn Ile Pro Tyr Pro Thr His Leu Leu Ser Cys
515 520 525

Gly Leu Asp Asn Thr Ile Lys Leu Trp Asp Val Lys Thr Gly Lys Cys
530 535 540

Ile Arg Thr Gln Phe Gly His Val Glu Gly Val Trp Asp Ile Ala Ala
545 550 555 560

Asp Asn Phe Arg Ile Ile Ser Gly Ser His Asp Gly Ser Ile Lys Val
565 570 575

Trp Asp Leu Gln Ser Gly Lys Cys Met His Thr Phe Asn Gly Arg Arg
580 585 590

Leu Gln Arg Glu Thr Gln His Thr Gln Thr Gln Ser Leu Gly Asp Lys
595 600 605

Val Ala Pro Ile Ala Cys Val Cys Ile Gly Asp Ser Glu Cys Phe Ser
610 615 620

Gly Asp Glu Phe Gly Cys Val Lys Met Tyr Lys Phe Asp Leu Asn Asp
625 630 635 640

<210> 18
<211> 569
<212> PRT
<213> Mus musculus

<300>
<308> Genbank/NP_033901
<309> 1998-08-04
<313> (1) .. (569)

<400> 18

Met Asp Pro Ala Glu Ala Val Leu Gln Glu Lys Ala Leu Lys Phe Met
1 5 10 15

Asn Ser Ser Glu Arg Glu Asp Cys Asn Asn Gly Glu Pro Pro Arg Lys
20 25 30

Ile Ile Pro Glu Lys Asn Ser Leu Arg Gln Thr Tyr Asn Ser Cys Ala
 35 40 45

Arg Leu Cys Ile Asn Gln Glu Thr Val Cys Leu Thr Ser Thr Ala Met
 50 55 60

Lys Thr Glu Asn Cys Val Ala Lys Ala Lys Leu Ala Asn Gly Thr Ser
 65 70 75 80

Ser Met Ile Val Pro Lys Gln Arg Lys Leu Ser Ala Ser Tyr Glu Lys
 85 90 95

Glu Lys Glu Leu Cys Val Lys Tyr Phe Glu Gln Trp Ser Glu Ser Asp
 100 105 110

Gln Val Glu Phe Val Glu His Leu Ile Ser Gln Met Cys His Tyr Gln
 115 120 125

His Gly His Ile Asn Ser Tyr Leu Lys Pro Met Leu Gln Arg Asp Phe
 130 135 140

Ile Thr Ala Leu Pro Ala Arg Gly Leu Asp His Ile Ala Glu Asn Ile
 145 150 155 160

Leu Ser Tyr Leu Asp Ala Lys Ser Leu Cys Ala Ala Glu Leu Val Cys
 165 170 175

Lys Glu Trp Tyr Arg Val Thr Ser Asp Gly Met Leu Trp Lys Lys Leu
 180 185 190

Ile Glu Arg Met Val Arg Thr Asp Ser Leu Trp Arg Gly Leu Ala Glu
 195 200 205

Arg Arg Gly Trp Gly Gln Tyr Leu Phe Lys Asn Lys Pro Pro Asp Glu
 210 215 220

Asn Ala Pro Pro Asn Ser Phe Tyr Arg Ala Leu Tyr Pro Lys Ile Ile
 225 230 235 240

Gln Asp Ile Glu Thr Ile Glu Ser Asn Trp Arg Cys Gly Arg His Ser
 245 250 255

Leu Gln Arg Ile His Cys Arg Ser Glu Thr Ser Lys Gly Val Tyr Cys
 260 265 270

Leu Gln Tyr Asp Asp Gln Lys Ile Val Ser Gly Leu Arg Asp Asn Thr
 275 280 285

Ile Lys Ile Trp Asp Lys Ser Thr Leu Glu Cys Lys Arg Ile Leu Thr
 290 295 300

Gly His Thr Gly Ser Val Leu Cys Leu Gln Tyr Asp Glu Arg Val Ile
 305 310 315 320

Ile Thr Gly Ser Ser Asp Ser Thr Val Arg Val Trp Asp Val Asn Ala
 325 330 335

Gly Glu Met Leu Asn Thr Leu Ile His His Cys Glu Ala Val Leu His
 340 345 350

Leu Arg Phe Asn Asn Gly Met Met Val Thr Cys Ser Lys Asp Arg Ser
 355 360 365

Ile Ala Val Trp Asp Met Ala Ser Pro Thr Asp Ile Thr Leu Arg Arg
 370 375 380

Val Leu Val Gly His Arg Ala Ala Val Asn Val Val Asp Phe Asp Asp
 385 390 395 400

Lys Tyr Ile Val Ser Ala Ser Gly Asp Arg Thr Ile Lys Val Trp Asn
 405 410 415

Thr Ser Thr Cys Glu Phe Val Arg Thr Leu Asn Gly His Lys Arg Gly
 420 425 430

Ile Ala Cys Leu Gln Tyr Arg Asp Arg Leu Val Val Ser Gly Ser Ser
 435 440 445

Asp Asn Thr Ile Arg Leu Trp Asp Ile Glu Cys Gly Ala Cys Leu Arg
 450 455 460

Val Leu Glu Gly His Glu Glu Leu Val Arg Cys Ile Arg Phe Asp Asn
 465 470 475 480

Lys Arg Ile Val Ser Gly Ala Tyr Asp Gly Lys Ile Lys Val Trp Asp
 485 490 495

Leu Met Ala Ala Leu Asp Pro Arg Ala Pro Ala Gly Thr Leu Cys Leu
 500 505 510

Arg Thr Leu Val Glu His Ser Gly Arg Val Phe Arg Leu Gln Phe Asp
515 520 525

Glu Phe Gln Ile Val Ser Ser Ser His Asp Asp Thr Ile Leu Ile Trp
530 535 540

Asp Phe Leu Asn Asp Pro Ala Ala His Ala Glu Pro Pro Arg Ser Pro
545 550 555 560

Ser Arg Thr Tyr Thr Tyr Ile Ser Arg
565

<210> 19
<211> 5
<212> PRT
<213> Peptide Motif

<220>
<221> misc_feature
<222> (1)..(1)
<223> wherein Xaa can be Leu, Pro, or Ile

<220>
<221> DOMAIN
<222> (1)..(5)
<223> Cdc4 Phospho-Degron motif

<220>
<221> misc_feature
<222> (2)..(2)
<223> wherein Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (5)..(5)
<223> wherein Xaa can be any naturally occurring amino acid except
basic and bulky hydrophobic amino acids

<220>
<221> misc_feature
<222> (5)..(5)
<223> wherein Xaa can be any naturally occurring amino acid

<400> 19

Xaa Xaa Pro Thr Xaa
1 5

<210> 20
<211> 8
<212> PRT
<213> Peptide Motif

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<220>
<221> misc_feature
<222> (1)..(1)
<223> wherein Xaa can be Leu, Pro, or Ile

<220>
<221> DOMAIN
<222> (1)..(8)
<223> Cdc4 Phospho-Degron motif

<220>
<221> misc_feature
<222> (2)..(2)
<223> wherein Xaa can be Leu, Ile, Val, or Pro

<220>
<221> misc_feature
<222> (5)..(5)
<223> wherein Xaa can be any naturally occurring amino acid except
        basic and bulky hydrophobic amino acids

<220>
<221> misc_feature
<222> (6)..(6)
<223> wherein Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (7)..(7)
<223> wherein Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (8)..(8)
<223> wherein Xaa can be any naturally occurring amino acid

<400> 20

Xaa Xaa Thr Pro Xaa Xaa Xaa Xaa
1           5

<210> 21
<211> 4
<212> PRT
<213> Peptide Motif

<220>
<221> misc_feature
<222> (1)..(1)
<223> wherein Xaa can be Leu, Gly or Thr

<220>
<221> DOMAIN
<222> (1)..(4)
<223> Cdc4 Phospho-Degron motif

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<400> 21

Xaa Pro Thr Pro
1

<210> 22

<211> 779

<212> PRT

<213> *Saccharomyces cerevisiae*

<300>

<308> Genbank/S56245

<309> 1993-05-07

<313> (1)..(51)

<400> 22

Met Gly Ser Phe Pro Leu Ala Glu Phe Pro Leu Arg Asp Ile Pro Val
1 5 10 15

Pro Tyr Ser Tyr Arg Val Ser Gly Gly Ile Ala Ser Ser Gly Ser Val
20 25 30

Thr Ala Leu Val Thr Ala Ala Gly Thr His Arg Asn Ser Ser Thr Ala
35 40 45

Lys Thr Val Glu Thr Glu Asp Gly Glu Glu Asp Ile Asp Glu Tyr Gln
50 55 60

Arg Lys Arg Ala Ala Gly Ser Gly Glu Ser Thr Pro Glu Arg Ser Asp
65 70 75 80

Phe Lys Arg Val Lys His Asp Asn His Lys Thr Leu His Pro Val Asn
85 90 95

Leu Gln Asn Thr Gly Ala Ala Ser Val Asp Asn Asp Gly Leu His Asn
100 105 110

Leu Thr Asp Ile Ser Asn Asp Ala Glu Lys Leu Leu Met Ser Val Asp
115 120 125

Asp Gly Ser Ala Ala Pro Ser Thr Leu Ser Val Asn Met Gly Val Ala
130 135 140

Ser His Asn Val Ala Ala Pro Thr Thr Val Asn Ala Ala Thr Ile Thr
145 150 155 160

Gly Ser Asp Val Ser Asn Asn Val Asn Ser Ala Thr Ile Asn Asn Pro
165 170 175

Met Glu Glu Gly Ala Leu Pro Leu Ser Pro Thr Ala Ser Ser Pro Gly
180 185 190

Thr Thr Thr Pro Leu Ala Lys Thr Thr Lys Thr Ile Asn Asn Asn Asn
195 200 205

Asn Ile Ala Asp Leu Ile Glu Ser Lys Asp Ser Ile Ile Ser Pro Glu
210 215 220

Tyr Leu Ser Asp Glu Ile Phe Ser Ala Ile Asn Asn Asn Leu Pro His
225 230 235 240

Ala Tyr Phe Lys Asn Leu Leu Phe Arg Leu Val Ala Asn Met Asp Arg
245 250 255

Ser Glu Leu Ser Asp Leu Gly Thr Leu Ile Lys Asp Asn Leu Lys Arg
260 265 270

Asp Leu Ile Thr Ser Leu Pro Phe Glu Ile Ser Leu Lys Ile Phe Asn
275 280 285

Tyr Leu Gln Phe Glu Asp Ile Ile Asn Ser Leu Gly Val Ser Gln Asn
290 295 300

Trp Asn Lys Ile Ile Arg Lys Ser Thr Ser Leu Trp Lys Lys Leu Leu
305 310 315 320

Ile Ser Glu Asn Phe Val Ser Pro Lys Gly Phe Asn Ser Leu Asn Leu
325 330 335

Lys Leu Ser Gln Lys Tyr Pro Lys Leu Ser Gln Gln Asp Arg Leu Arg
340 345 350

Leu Ser Phe Leu Glu Asn Ile Phe Ile Leu Lys Asn Trp Tyr Asn Pro
355 360 365

Lys Phe Val Pro Gln Arg Thr Thr Leu Arg Gly His Met Thr Ser Val
370 375 380

Ile Thr Cys Leu Gln Phe Glu Asp Asn Tyr Val Ile Thr Gly Ala Asp
385 390 395 400

Asp Lys Met Ile Arg Val Tyr Asp Ser Ile Asn Lys Lys Phe Leu Leu
405 410 415

Gln Leu Ser Gly His Asp Gly Gly Val Trp Ala Leu Lys Tyr Ala His
420 425 430

Gly Gly Ile Leu Val Ser Gly Ser Thr Asp Arg Thr Val Arg Val Trp
435 440 445

Asp Ile Lys Lys Gly Cys Cys Thr His Val Phe Lys Gly His Asn Ser
450 455 460

Thr Val Arg Cys Leu Asp Ile Val Glu Tyr Lys Asn Ile Lys Tyr Ile
465 470 475 480

Val Thr Gly Ser Arg Asp Asn Thr Leu His Val Trp Lys Leu Pro Lys
485 490 495

Glu Ser Ser Val Pro Asp His Gly Glu Glu His Asp Tyr Pro Leu Val
500 505 510

Phe His Thr Pro Glu Glu Asn Pro Tyr Phe Val Gly Val Leu Arg Gly
515 520 525

His Met Ala Ser Val Arg Thr Val Ser Gly His Gly Asn Ile Val Val
530 535 540

Ser Gly Ser Tyr Asp Asn Thr Leu Ile Val Trp Asp Val Ala Gln Met
545 550 555 560

Lys Cys Leu Tyr Ile Leu Ser Gly His Thr Asp Arg Ile Tyr Ser Thr
565 570 575

Ile Tyr Asp His Glu Arg Lys Arg Cys Ile Ser Ala Ser Met Asp Thr
580 585 590

Thr Ile Arg Ile Trp Asp Leu Glu Asn Ile Trp Asn Asn Gly Glu Cys
595 600 605

Ser Tyr Ala Thr Asn Ser Ala Ser Pro Cys Ala Lys Ile Leu Gly Ala
610 615 620

Met Tyr Thr Leu Gln Gly His Thr Ala Leu Val Gly Leu Leu Arg Leu
625 630 635 640

Ser Asp Lys Phe Leu Val Ser Ala Ala Ala Asp Gly Ser Ile Arg Gly
645 650 655

Trp Asp Ala Asn Asp Tyr Ser Arg Lys Phe Ser Tyr His His Thr Asn
660 665 670

Leu Ser Ala Ile Thr Thr Phe Tyr Val Ser Asp Asn Ile Leu Val Ser
675 680 685

Gly Ser Glu Asn Gln Phe Asn Ile Tyr Asn Leu Arg Ser Gly Lys Leu
690 695 700

Val His Ala Asn Ile Leu Lys Asp Ala Asp Gln Ile Trp Ser Val Asn
705 710 715 720

Phe Lys Gly Lys Thr Leu Val Ala Ala Val Glu Lys Asp Gly Gln Ser
725 730 735

Phe Leu Glu Ile Leu Asp Phe Ser Lys Ala Ser Lys Ile Asn Tyr Val
740 745 750

Ser Asn Pro Val Asn Ser Ser Ser Ser Ser Leu Glu Ser Ile Ser Thr
755 760 765

Ser Leu Gly Leu Thr Arg Thr Thr Ile Ile Pro
770 775

<210> 23
<211> 684
<212> PRT
<213> Candida albicans

<300>
<308> Genbank/CAA65538
<309> 1996-04-04
<313> (1) .. (684)

<400> 23

Met Pro Ser Cys Asp Asp Thr Ala Ser Ser Asp Thr Asp Cys Gln Ser
1 5 10 15

Gln Val Ser Ser Thr Ala His Leu His Ser Tyr Arg Ser Asn Gly Leu
20 25 30

Val Glu Pro Pro Ser Lys Arg Arg Leu Thr Thr Thr Asn Glu Thr Ser
35 40 45

Leu Ser Ser Ala Gly Ala Thr Thr Phe Gln Ile Glu Ser Pro Gly Ser
50 55 60

Ile Ser Ala Ile Thr Thr Asn Asn Ser Thr Thr Ser Ala Gly Asp Ser
65 70 75 80

Asn Asn Ser Asn Ser Phe Ser Asp Gln His Ser Arg His Pro Arg Thr
85 90 95

Pro Asn Ala Met Asn Ser Pro Thr His Thr Pro Ile Ser Asp Ile Glu
100 105 110

Glu Asp Pro Ile Gln Gln Leu Pro Leu Pro Ser Pro Ser Ala Ser Pro
115 120 125

Ile Gln Ser Asp Thr Glu Asn Glu His Val Thr Thr Pro Asp Ser Leu
130 135 140

Gln Gly Lys Ala Asn Leu Asp Ser Ile Glu Asn Val Met Ser Asn Glu
145 150 155 160

Pro Thr Thr Gln Ser Glu Leu Val Asp Leu Val Thr Lys Leu Ser Gly
165 170 175

Phe Leu Ser Glu Ala Asn Gln Asn His Leu Val Phe Lys Leu Leu Gln
180 185 190

Lys Thr Thr Arg Pro Thr Leu Ser Thr Phe Asn Asn Leu Ile Asn Asn
195 200 205

Ser Leu Lys Arg Asp Ile Leu Ser Asn Val Pro Phe Glu Val Thr Met
210 215 220

Lys Ile Leu Ser Tyr Leu Asp Tyr Lys Thr Leu Leu Ser Val Ala Gln
225 230 235 240

Val Cys Lys Lys Trp Phe Asp Ile Ile Asn Asn Pro Asp Thr Trp Ile
245 250 255

Lys Leu Leu Lys Arg Asp Lys Leu Ile Thr Asp Asp Ala Val Ile Lys
260 265 270

Tyr Glu Leu Gln Tyr Pro Asp Gln Leu Leu Arg Glu Trp Ser Thr Leu
275 280 285

Pro Glu Ile Asn Ser Ala Gln Val Leu Tyr Lys Lys Arg Lys Ile Ile
290 295 300

Val Asn Arg Trp Met Asp Pro Lys Phe Lys Pro His Arg Ile Ser Val
 305 310 315 320

Ser Gly His Gly Asn Lys Val Val Thr Cys Leu Gln His Asp Asp Glu
 325 330 335

Lys Val Val Thr Gly Val Asp Asp Lys Cys Ile Ser Ile Tyr Ser Thr
 340 345 350

Gln Thr Gly Gln Leu Met Lys Val Leu Glu Gly His Glu Gly Gly Val
 355 360 365

Trp Ala Leu Lys Tyr Thr Gly Asn Thr Leu Val Thr Gly Ser Thr Asp
 370 375 380

Arg Thr Val Arg Val Trp Asn Met Lys Thr Gly Gln Cys Thr His Ile
 385 390 395 400

Phe Arg Gly His Thr Ser Thr Ile Arg Cys Leu Asp Ile Ile His Pro
 405 410 415

Ala Val Ile Gly Lys Asn Gln Asp Gly Glu Asp Ile Val Phe Pro Glu
 420 425 430

Tyr Pro Leu Leu Ile Thr Gly Ser Arg Asp His Asn Ile His Val Trp
 435 440 445

Lys Leu Pro Val Val Asp Asp Ser Gln Asp Tyr Ile Glu Thr Phe Glu
 450 455 460

Gly Glu Phe Asp Asn Pro Tyr Leu Ile Ala Val Leu Ser Gly His Thr
 465 470 475 480

Gln Ser Val Arg Ser Ile Ser Gly Tyr Gly Asn Ile Ile Ile Ser Gly
 485 490 495

Ser Tyr Asp Ser Thr Val Arg Val Trp Asp Leu Leu Asp Asp Gly His
 500 505 510

Cys Thr His Val Leu Gln Gly His Leu Asp Arg Val Tyr Ser Thr Ala
 515 520 525

Ile Asp Phe His Ser Lys Thr Cys Phe Ser Gly Ser Met Asp Ser Asn
 530 535 540

Ile Asn Val Trp Asn Phe Glu Thr Gly Glu Leu Lys Lys Val Leu Val
 545 550 555 560

Gly His Ala Ser Leu Val Gly Leu Leu Asp Leu Val Asp Asp Val Leu
 565 570 575

Val Ser Ala Ala Ala Asp Ala Thr Leu Arg Ile Trp Asp Ala Lys Thr
 580 585 590

Gly Glu Leu Arg Ser Lys Leu Lys Gly His Gly Ala Ala Ile Thr Cys
 595 600 605

Phe Glu His Asp Gly Leu Arg Val Val Ser Gly Ser Glu Lys Met Leu
 610 615 620

Lys Leu Trp Asn Val Glu Lys Gly Thr Phe Ala Arg Asp Leu Leu Ser
 625 630 635 640

Asp Val Thr Gly Gly Ile Trp Gln Val Arg Phe Asp Tyr Lys Arg Cys
 645 650 655

Val Ala Ala Val Gln Arg Ile Ile Asn Glu Asp Glu Gly Glu Thr Phe
 660 665 670

Ile Glu Ile Leu Asp Phe Ser Gln Pro Leu Leu Gln
 675 680

<210> 24
 <211> 707
 <212> PRT
 <213> Homo sapiens

<300>
 <308> Genbank/AAL07271
 <309> 2001-08-30
 <313> (1)..(707)

<400> 24

Met Asn Gln Glu Leu Leu Ser Val Gly Ser Lys Arg Arg Arg Thr Gly
 1 5 10 15

Gly Ser Leu Arg Gly Asn Pro Ser Ser Ser Gln Val Asp Glu Glu Gln
 20 25 30

Met Asn Arg Val Val Glu Glu Glu Gln Gln Gln Gln Leu Arg Gln Gln
 35 40 45

Glu Glu Glu His Thr Ala Arg Asn Gly Glu Val Val Gly Val Glu Pro
 50 55 60

Arg Pro Gly Gly Gln Asn Asp Ser Gln Gln Gly Gln Leu Glu Glu Asn
 65 70 75 80

Asn Asn Arg Phe Ile Ser Val Asp Glu Asp Ser Ser Gly Asn Gln Glu
 85 90 95

Glu Gln Glu Glu Asp Glu Glu His Ala Gly Glu Gln Asp Glu Glu Asp
 100 105 110

Glu Glu Glu Glu Glu Met Asp Gln Glu Ser Asp Asp Phe Asp Gln Ser
 115 120 125

Asp Asp Ser Ser Arg Glu Asp Glu His Thr His Thr Asn Ser Val Thr
 130 135 140

Asn Ser Ser Ser Ile Val Asp Leu Pro Val His Gln Leu Ser Ser Pro
 145 150 155 160

Phe Tyr Thr Lys Thr Thr Lys Met Lys Arg Lys Leu Asp His Gly Ser
 165 170 175

Glu Val Arg Ser Phe Ser Leu Gly Lys Lys Pro Cys Lys Val Ser Glu
 180 185 190

Tyr Thr Ser Thr Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr
 195 200 205

Phe Gly Asp Leu Arg Ala Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg
 210 215 220

Ile Thr Ser Val Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met
 225 230 235 240

Phe Gln Ser Trp Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu
 245 250 255

Ile Asp Ser Cys Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile
 260 265 270

Glu Pro Gln Phe Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu
 275 280 285

Ala Leu Tyr Val Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala
290 295 300

Ala Gln Thr Cys Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu
305 310 315 320

Trp Arg Glu Lys Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile
325 330 335

Lys Arg Arg Lys Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys
340 345 350

Ser Ala Tyr Ile Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly
355 360 365

Glu Leu Lys Ser Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile
370 375 380

Thr Cys Leu Gln Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asp
385 390 395 400

Asn Thr Leu Lys Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr
405 410 415

Leu Val Gly His Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn
420 425 430

Ile Ile Ile Ser Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala
435 440 445

Glu Thr Gly Glu Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val
450 455 460

Arg Cys Met His Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp
465 470 475 480

Ala Thr Leu Arg Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val
485 490 495

Leu Met Gly His Val Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Arg
500 505 510

Arg Val Val Ser Gly Ala Tyr Asp Phe Met Val Lys Val Trp Asp Pro
515 520 525

Glu Thr Glu Thr Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val
530 535 540

Tyr Ser Leu Gln Phe Asp Gly Ile His Val Val Ser Gly Ser Leu Asp
545 550 555 560

Thr Ser Ile Arg Val Trp Asp Val Glu Thr Gly Asn Cys Ile His Thr
565 570 575

Leu Thr Gly His Gln Ser Leu Thr Ser Gly Met Glu Leu Lys Asp Asn
580 585 590

Ile Leu Val Ser Gly Asn Ala Asp Ser Thr Val Lys Ile Trp Asp Ile
595 600 605

Lys Thr Gly Gln Cys Leu Gln Thr Leu Gln Gly Pro Asn Lys His Gln
610 615 620

Ser Ala Val Thr Cys Leu Gln Phe Asn Lys Asn Phe Val Ile Thr Ser
625 630 635 640

Ser Asp Asp Gly Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe
645 650 655

Ile Arg Asn Leu Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val
660 665 670

Trp Arg Ile Arg Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser
675 680 685

Arg Asn Gly Thr Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp Val
690 695 700

Asp Met Lys
705

<210> 25
<211> 587
<212> PRT
<213> Caenorhabditis elegans

<300>
<308> Genbank/AAC47809
<309> 1997-12-12
<313> (1) .. (587)

<400> 25

Met Trp Pro Arg Asn Asp Val His Met Asp Asp Gly Ser Met Thr Pro
1 5 10 15

Glu Asp Gln Glu Pro Val Thr Asp Asn Asp Met Glu Tyr Asn Asp Asn
20 25 30

Gly Glu Glu Ser Ser Tyr Ser Asn Gly Ser Ser Ser Ser Tyr Asn Ala
35 40 45

Asp Lys Leu Ser Ser Ser Arg Pro Leu Gln His Lys Leu Asp Leu Ser
50 55 60

Ala Ser Pro Ser Arg Asn Asn Asp Leu Asn Pro Arg Val Glu His Leu
65 70 75 80

Ile Ala Leu Phe Lys Asp Leu Ser Ser Ala Glu Gln Met Asp Ala Phe
85 90 95

Thr Arg Leu Leu Gln Glu Ser Asn Met Thr Asn Ile Arg Gln Leu Arg
100 105 110

Ala Ile Ile Glu Pro His Phe Gln Arg Asp Phe Leu Ser Cys Leu Pro
115 120 125

Val Glu Leu Gly Met Lys Ile Leu His Asn Leu Thr Gly Tyr Asp Leu
130 135 140

Leu Lys Val Ala Gln Val Ser Lys Asn Trp Lys Leu Ile Ser Glu Ile
145 150 155 160

Asp Lys Ile Trp Lys Ser Leu Gly Val Glu Glu Phe Lys His His Pro
165 170 175

Asp Pro Thr Asp Arg Val Thr Gly Ala Trp Gln Gly Thr Ala Ile Ala
180 185 190

Ala Gly Val Thr Ile Pro Asp His Ile Gln Pro Cys Asp Leu Asn Val
195 200 205

His Arg Phe Leu Lys Leu Gln Lys Phe Gly Asp Ile Phe Glu Arg Ala
210 215 220

Ala Asp Lys Ser Arg Tyr Leu Arg Ala Asp Lys Ile Glu Lys Asn Trp
225 230 235 240

Asn Ala Asn Pro Ile Met Gly Ser Ala Val Leu Arg Gly His Glu Asp
245 250 255

His Val Ile Thr Cys Met Gln Ile His Asp Asp Val Leu Val Thr Gly
260 265 270

Ser Asp Asp Asn Thr Leu Lys Val Trp Cys Ile Asp Lys Gly Glu Val
275 280 285

Met Tyr Thr Leu Val Gly His Thr Gly Gly Val Trp Thr Ser Gln Ile
290 295 300

Ser Gln Cys Gly Arg Tyr Ile Val Ser Gly Ser Thr Asp Arg Thr Val
305 310 315 320

Lys Val Trp Ser Thr Val Asp Gly Ser Leu Leu His Thr Leu Gln Gly
325 330 335

His Thr Ser Thr Val Arg Cys Met Ala Met Ala Gly Ser Ile Leu Val
340 345 350

Thr Gly Ser Arg Asp Thr Thr Leu Arg Val Trp Asp Val Glu Ser Gly
355 360 365

Arg His Leu Ala Thr Leu His Gly His His Ala Ala Val Arg Cys Val
370 375 380

Gln Phe Asp Gly Thr Thr Val Val Ser Gly Gly Tyr Asp Phe Thr Val
385 390 395 400

Lys Ile Trp Asn Ala His Thr Gly Arg Cys Ile Arg Thr Leu Thr Gly
405 410 415

His Asn Asn Arg Val Tyr Ser Leu Leu Phe Glu Ser Glu Arg Ser Ile
420 425 430

Val Cys Ser Gly Ser Leu Asp Thr Ser Ile Arg Val Trp Asp Phe Thr
435 440 445

Arg Pro Glu Gly Gln Glu Cys Val Ala Leu Leu Gln Gly His Thr Ser
450 455 460

Leu Thr Ser Gly Met Gln Leu Arg Gly Asn Ile Leu Val Ser Cys Asn
465 470 475 480

Ala Asp Ser His Val Arg Val Trp Asp Ile His Glu Gly Thr Cys Val
485 490 495

His Met Leu Ser Gly His Arg Ser Ala Ile Thr Ser Leu Gln Trp Phe
500 505 510

Gly Arg Asn Met Val Ala Thr Ser Ser Asp Asp Gly Thr Val Lys Leu
515 520 525

Trp Asp Ile Glu Arg Gly Ala Leu Ile Arg Asp Leu Val Thr Leu Asp
530 535 540

Ser Gly Gly Asn Gly Gly Cys Ile Trp Arg Leu Cys Ser Thr Ser Thr
545 550 555 560

Met Leu Ala Cys Ala Val Gly Ser Arg Asn Asn Thr Glu Glu Thr Lys
565 570 575

Val Ile Leu Leu Asp Phe Asp Ala Val Tyr Pro
580 585

<210> 26
<211> 627
<212> PRT
<213> Homo sapiens

<300>
<308> Genbank/AAK57547
<309> 2001-08-22
<313> (1) .. (627)

<400> 26

Met Cys Val Pro Arg Ser Gly Leu Ile Leu Ser Cys Ile Cys Leu Tyr
1 5 10 15

Cys Gly Val Leu Leu Pro Val Leu Leu Pro Asn Leu Pro Phe Leu Thr
20 25 30

Cys Leu Ser Met Ser Thr Leu Glu Ser Val Thr Tyr Leu Pro Glu Lys
35 40 45

Gly Leu Tyr Cys Gln Arg Leu Pro Ser Ser Arg Thr His Gly Gly Thr
50 55 60

Glu Ser Leu Lys Gly Lys Asn Thr Glu Asn Met Gly Phe Tyr Gly Thr
65 70 75 80

Leu Lys Met Ile Phe Tyr Lys Met Lys Arg Lys Leu Asp His Gly Ser
85 90 95

Glu Val Arg Ser Phe Ser Leu Gly Lys Lys Pro Cys Lys Val Ser Glu
100 105 110

Tyr Thr Ser Thr Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr
115 120 125

Phe Gly Asp Leu Arg Ala Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg
130 135 140

Ile Thr Ser Val Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met
145 150 155 160

Phe Gln Ser Trp Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu
165 170 175

Ile Asp Ser Cys Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile
180 185 190

Glu Pro Gln Phe Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu
195 200 205

Ala Leu Tyr Val Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala
210 215 220

Ala Gln Thr Cys Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu
225 230 235 240

Trp Arg Glu Lys Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile
245 250 255

Lys Arg Arg Lys Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys
260 265 270

Ser Ala Tyr Ile Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly
275 280 285

Glu Leu Lys Ser Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile
290 295 300

Thr Cys Leu Gln Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asp
305 310 315 320

Asn Thr Leu Lys Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr
325 330 335

Leu Val Gly His Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn
340 345 350

Ile Ile Ile Ser Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala
355 360 365

Glu Thr Gly Glu Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val
370 375 380

Arg Cys Met His Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp
385 390 395 400

Ala Thr Leu Arg Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val
405 410 415

Leu Met Gly His Val Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Arg
420 425 430

Arg Val Val Ser Gly Ala Tyr Asp Phe Met Val Lys Val Trp Asp Pro
435 440 445

Glu Thr Glu Thr Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val
450 455 460

Tyr Ser Leu Gln Phe Asp Gly Ile His Val Val Ser Gly Ser Leu Asp
465 470 475 480

Thr Ser Ile Arg Val Trp Asp Val Glu Thr Gly Asn Cys Ile His Thr
485 490 495

Leu Thr Gly His Gln Ser Leu Thr Ser Gly Met Glu Leu Lys Asp Asn
500 505 510

Ile Leu Val Ser Gly Asn Ala Asp Ser Thr Val Lys Ile Trp Asp Ile
515 520 525

Lys Thr Gly Gln Cys Leu Gln Thr Leu Gln Gly Pro Asn Lys His Gln
530 535 540

Ser Ala Val Thr Cys Leu Gln Phe Asn Lys Asn Phe Val Ile Thr Ser
545 550 555 560

Ser Asp Asp Gly Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe
565 570 575

Ile Arg Asn Leu Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val
580 585 590

Trp Arg Ile Arg Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser
595 600 605

Arg Asn Gly Thr Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp Val
610 615 620

Asp Met Lys
625

<210> 27
<211> 224
<212> PRT
<213> Homo sapiens

<400> 27

Met Ala Val Gly Asn Ile Asn Glu Leu Pro Glu Asn Ile Leu Leu Glu
1 5 10 15

Leu Phe Thr His Val Pro Ala Arg Gln Leu Leu Leu Asn Cys Arg Leu
20 25 30

Val Cys Ser Leu Trp Arg Asp Leu Ile Asp Leu Val Thr Leu Trp Lys
35 40 45

Arg Lys Cys Leu Arg Glu Gly Phe Ile Thr Glu Asp Trp Asp Gln Pro
50 55 60

Val Ala Asp Trp Lys Ile Phe Tyr Phe Leu Arg Ser Leu His Arg Asn
65 70 75 80

Leu Leu His Asn Pro Cys Ala Glu Glu Gly Phe Glu Phe Trp Ser Leu
85 90 95

Asp Val Asn Gly Gly Asp Glu Trp Lys Val Glu Asp Leu Ser Arg Asp
100 105 110

Gln Arg Lys Glu Phe Pro Asn Asp Gln Val Arg Ser Gln Ala Arg Leu
115 120 125

Arg Val Gln Val Pro Ala Val Arg Ser Ala Pro Val Val Arg Ala Arg
 130 135 140

Ala Ser Gly Asp Leu Pro Ala Arg Pro Gly Asp His Pro Ala Glu Glu
 145 150 155 160

Arg Cys Gln Val Glu Gly Gly Leu Pro His Ile Leu Gln Leu Pro Ala
 165 170 175

Arg Arg Pro Leu His Leu Val Ser Ala Arg Arg Arg Gly His Ser Leu
 180 185 190

Leu Gly Arg Leu Val Arg Pro Glu Gly His Gln Gln Gln His His His
 195 200 205

Arg Ala Pro Ala Ala Leu Thr Pro Pro Glu Pro Pro Ser Ala Glu Pro
 210 215 220

<210> 28
 <211> 815
 <212> PRT
 <213> Saccharomyces cerevisiae

<300>
 <308> Genbank/AAB38821
 <309> 1996-12-17
 <313> (1) .. (815)

<400> 28

Met Ser Glu Thr Leu Pro Arg Ser Asp Asp Leu Glu Ala Thr Trp Asn
 1 5 10 15

Phe Ile Glu Pro Gly Ile Asn Gln Ile Leu Gly Asn Glu Lys Asn Gln
 20 25 30

Ala Ser Thr Ser Lys Arg Val Tyr Lys Ile Leu Ser Pro Thr Met Tyr
 35 40 45

Met Glu Val Tyr Thr Ala Ile Tyr Asn Tyr Cys Val Asn Lys Ser Arg
 50 55 60

Ser Ser Gly His Phe Ser Thr Asp Ser Arg Thr Gly Gln Ser Thr Ile
 65 70 75 80

Leu Val Gly Ser Glu Ile Tyr Glu Lys Leu Lys Asn Tyr Leu Lys Asn
 85 90 95

Tyr Ile Leu Asn Phe Lys Gln Ser Asn Ser Glu Thr Phe Leu Gln Phe
100 105 110

Tyr Val Lys Arg Trp Lys Arg Phe Thr Ile Gly Ala Ile Phe Leu Asn
115 120 125

His Ala Phe Asp Tyr Met Asn Arg Tyr Trp Val Gln Lys Glu Arg Ser
130 135 140

Asp Gly Lys Arg His Ile Phe Asp Val Asn Thr Leu Cys Leu Met Thr
145 150 155 160

Trp Lys Glu Val Met Phe Asp Pro Ser Lys Asp Val Leu Ile Asn Glu
165 170 175

Leu Leu Asp Gln Val Thr Leu Gly Arg Glu Gly Gln Ile Ile Gln Arg
180 185 190

Ser Asn Ile Ser Thr Ala Ile Lys Ser Leu Val Ala Leu Gly Ile Asp
195 200 205

Pro Gln Asp Leu Lys Lys Leu Asn Leu Asn Val Tyr Ile Gln Val Phe
210 215 220

Glu Lys Pro Phe Leu Lys Lys Thr Gln Glu Tyr Tyr Thr Gln Tyr Thr
225 230 235 240

Asn Asp Tyr Leu Glu Lys His Ser Val Thr Glu Tyr Ile Phe Glu Ala
245 250 255

His Glu Ile Ile Lys Arg Glu Glu Lys Ala Met Thr Ile Tyr Trp Asp
260 265 270

Asp His Thr Lys Lys Pro Leu Ser Met Ala Leu Asn Lys Val Leu Ile
275 280 285

Thr Asp His Ile Glu Lys Leu Glu Asn Glu Phe Val Val Leu Leu Asp
290 295 300

Ala Arg Asp Ile Glu Lys Ile Thr Ser Leu Tyr Ala Leu Ile Arg Arg
305 310 315 320

Asp Phe Thr Leu Ile Pro Arg Met Ala Ser Val Phe Glu Asn Tyr Val
325 330 335

Lys Lys Thr Gly Glu Asn Glu Ile Ser Ser Leu Leu Ala Met His Lys
340 345 350

His Asn Ile Met Lys Asn Glu Asn Ala Asn Pro Lys Lys Leu Ala Leu
355 360 365

Met Thr Ala His Ser Leu Ser Pro Lys Asp Tyr Ile Lys Lys Leu Leu
370 375 380

Glu Val His Asp Ile Phe Ser Lys Ile Phe Asn Glu Ser Phe Pro Asp
385 390 395 400

Asp Ile Pro Leu Ala Lys Ala Leu Asp Asn Ala Cys Gly Ala Phe Ile
405 410 415

Asn Ile Asn Glu Phe Ala Leu Pro Ala Gly Ser Pro Lys Ser Ala Thr
420 425 430

Ser Lys Thr Ser Glu Met Leu Ala Lys Tyr Ser Asp Ile Leu Leu Lys
435 440 445

Lys Ala Thr Lys Pro Glu Val Ala Ser Asp Met Ser Asp Glu Asp Ile
450 455 460

Ile Thr Ile Phe Lys Tyr Leu Thr Asp Lys Asp Ala Phe Glu Thr His
465 470 475 480

Tyr Arg Arg Leu Phe Ala Lys Arg Leu Ile His Gly Thr Ser Thr Ser
485 490 495

Ala Glu Asp Glu Glu Asn Ile Ile Gln Arg Leu Gln Ala Ala Asn Ser
500 505 510

Met Glu Tyr Thr Gly Lys Ile Thr Lys Met Phe Gln Asp Ile Arg Leu
515 520 525

Ser Lys Ile Leu Glu Asp Asp Phe Ala Val Ala Leu Lys Asn Glu Pro
530 535 540

Asp Tyr Ser Lys Ala Lys Tyr Pro Asp Leu Gln Pro Phe Val Leu Ala
545 550 555 560

Glu Asn Met Trp Pro Phe Ser Tyr Gln Glu Val Glu Phe Lys Leu Pro
565 570 575

Lys Glu Leu Val Pro Ser His Glu Lys Leu Lys Glu Ser Tyr Ser Gln
580 585 590

Lys His Asn Gly Arg Ile Leu Lys Trp Leu Trp Pro Leu Cys Arg Gly
595 600 605

Glu Leu Lys Ala Asp Ile Gly Lys Pro Gly Arg Met Pro Phe Asn Phe
610 615 620

Thr Val Thr Leu Phe Gln Met Ala Ile Leu Leu Leu Tyr Asn Asp Ala
625 630 635 640

Asp Val Leu Thr Leu Glu Asn Ile Gln Glu Gly Thr Ser Leu Thr Ile
645 650 655

Gln His Ile Ala Ala Ala Met Val Pro Phe Ile Lys Phe Lys Leu Ile
660 665 670

Gln Gln Val Pro Pro Gly Leu Asp Ala Leu Val Lys Pro Glu Thr Gln
675 680 685

Phe Lys Leu Ser Arg Pro Tyr Lys Ala Leu Lys Thr Asn Ile Asn Phe
690 695 700

Ala Ser Gly Val Lys Asn Asp Ile Leu Gln Ser Leu Ser Gly Gly Gly
705 710 715 720

His Asp Asn His Gly Asn Lys Leu Gly Asn Lys Arg Leu Thr Glu Asp
725 730 735

Glu Arg Ile Glu Lys Glu Leu Asn Thr Glu Arg Gln Ile Phe Leu Glu
740 745 750

Ala Cys Ile Val Arg Ile Met Lys Ala Lys Arg Asn Leu Pro His Thr
755 760 765

Thr Leu Val Asn Glu Cys Ile Ala Gln Ser His Gln Arg Phe Asn Ala
770 775 780

Lys Val Ser Met Val Lys Arg Ala Ile Asp Ser Leu Ile Gln Lys Gly
785 790 795 800

Tyr Leu Gln Arg Gly Asp Asp Gly Glu Ser Tyr Ala Tyr Leu Ala
805 810 815

<210> 29
 <211> 768
 <212> PRT
 <213> Homo sapiens

<300>
 <308> Genbank/AAC36304
 <309> 1998-09-19
 <313> (1)..(768)

<400> 29

Met Ser Asn Leu Ser Lys Gly Thr Gly Ser Arg Lys Asp Thr Lys Met
 1 5 10 15

Arg Ile Arg Ala Phe Pro Met Thr Met Asp Glu Lys Tyr Val Asn Ser
 20 25 30

Ile Trp Asp Leu Leu Lys Asn Ala Ile Gln Glu Ile Gln Arg Lys Asn
 35 40 45

Asn Ser Gly Leu Ser Phe Glu Glu Leu Tyr Arg Asn Ala Tyr Thr Met
 50 55 60

Val Leu His Lys His Gly Glu Lys Leu Tyr Thr Gly Leu Arg Glu Val
 65 70 75 80

Val Thr Glu His Leu Ile Asn Lys Val Arg Glu Asp Val Leu Asn Ser
 85 90 95

Leu Asn Asn Asn Phe Leu Gln Thr Leu Asn Gln Ala Trp Asn Asp His
 100 105 110

Gln Thr Ala Met Val Met Ile Arg Asp Ile Leu Met Tyr Met Asp Arg
 115 120 125

Val Tyr Val Gln Gln Asn Asn Val Glu Asn Val Tyr Asn Leu Gly Leu
 130 135 140

Ile Ile Phe Arg Asp Gln Val Val Arg Tyr Gly Cys Ile Arg Asp His
 145 150 155 160

Leu Arg Gln Thr Leu Leu Asp Met Ile Ala Arg Glu Arg Lys Gly Glu
 165 170 175

Val Val Asp Arg Gly Ala Ile Arg Asn Ala Cys Gln Met Leu Met Ile
 180 185 190

Leu Gly Leu Glu Gly Arg Ser Val Tyr Glu Glu Asp Phe Glu Ala Pro
195 200 205

Phe Leu Glu Met Ser Ala Glu Phe Phe Gln Met Glu Ser Gln Lys Phe
210 215 220

Leu Ala Glu Asn Ser Ala Ser Val Tyr Ile Lys Lys Val Glu Ala Arg
225 230 235 240

Ile Asn Glu Glu Ile Glu Arg Val Met His Cys Leu Asp Lys Ser Thr
245 250 255

Glu Glu Pro Ile Val Lys Val Val Glu Arg Glu Leu Ile Ser Lys His
260 265 270

Met Lys Thr Ile Val Glu Met Glu Asn Ser Gly Leu Val His Met Leu
275 280 285

Lys Asn Gly Lys Thr Glu Asp Leu Gly Cys Met Tyr Lys Leu Phe Ser
290 295 300

Arg Val Pro Asn Gly Leu Lys Thr Met Cys Glu Cys Met Ser Ser Tyr
305 310 315 320

Leu Arg Glu Gln Gly Lys Ala Leu Val Ser Glu Glu Gly Glu Gly Lys
325 330 335

Asn Pro Val Asp Tyr Ile Gln Gly Leu Leu Asp Leu Lys Ser Arg Phe
340 345 350

Asp Arg Phe Leu Leu Glu Ser Phe Asn Asn Asp Arg Leu Phe Lys Gln
355 360 365

Thr Ile Ala Gly Asp Phe Glu Tyr Phe Leu Asn Leu Asn Ser Arg Ser
370 375 380

Pro Glu Tyr Leu Ser Leu Phe Ile Asp Asp Lys Leu Lys Lys Gly Val
385 390 395 400

Lys Gly Leu Thr Glu Gln Glu Val Glu Thr Ile Leu Asp Lys Ala Met
405 410 415

Val Leu Phe Arg Phe Met Gln Glu Lys Asp Val Phe Glu Arg Tyr Tyr
420 425 430

Lys Gln His Leu Ala Arg Arg Leu Leu Thr Asn Lys Ser Val Ser Asp
 435 440 445

Asp Ser Glu Lys Asn Met Ile Ser Lys Leu Lys Thr Glu Cys Gly Cys
 450 455 460

Gln Phe Thr Ser Lys Leu Glu Gly Met Phe Arg Asp Met Ser Ile Ser
 465 470 475 480

Asn Thr Thr Met Asp Glu Phe Arg Gln His Leu Gln Ala Thr Gly Val
 485 490 495

Ser Leu Gly Gly Val Asp Leu Thr Val Arg Val Leu Thr Thr Gly Tyr
 500 505 510

Trp Pro Thr Gln Ser Ala Thr Pro Lys Cys Asn Ile Pro Pro Ala Pro
 515 520 525

Arg His Ala Phe Glu Ile Phe Arg Arg Phe Tyr Leu Ala Lys His Ser
 530 535 540

Gly Arg Gln Leu Thr Leu Gln His His Met Gly Ser Ala Asp Leu Asn
 545 550 555 560

Ala Thr Phe Tyr Gly Pro Val Lys Lys Glu Asp Gly Ser Glu Val Gly
 565 570 575

Val Gly Gly Ala Gln Val Thr Gly Ser Asn Thr Arg Lys His Ile Leu
 580 585 590

Gln Val Ser Thr Phe Gln Met Thr Ile Leu Met Leu Phe Asn Asn Arg
 595 600 605

Glu Lys Tyr Thr Phe Glu Glu Ile Gln Gln Glu Thr Asp Ile Pro Glu
 610 615 620

Arg Glu Leu Val Arg Ala Leu Gln Ser Leu Ala Cys Gly Lys Pro Thr
 625 630 635 640

Gln Arg Val Leu Thr Lys Glu Pro Lys Ser Lys Glu Ile Glu Asn Gly
 645 650 655

His Ile Phe Thr Val Asn Asp Gln Phe Thr Ser Lys Leu His Arg Val
 660 665 670

Lys Ile Gln Thr Val Ala Ala Lys Gln Gly Glu Ser Asp Pro Glu Arg
675 680 685

Lys Glu Thr Arg Gln Lys Val Asp Asp Asp Arg Lys His Glu Ile Glu
690 695 700

Ala Ala Ile Val Arg Ile Met Lys Ser Arg Lys Lys Met Gln His Asn
705 710 715 720

Val Leu Val Ala Glu Val Thr Gln Gln Leu Lys Ala Arg Phe Leu Pro
725 730 735

Ser Pro Val Val Ile Lys Lys Arg Ile Glu Gly Leu Ile Glu Arg Glu
740 745 750

Tyr Leu Ala Arg Thr Pro Glu Asp Arg Lys Val Tyr Thr Tyr Val Ala
755 760 765

<210> 30
<211> 745
<212> PRT
<213> Homo sapiens

<300>
<308> Genbank/ AAC51190
<309> 1997-04-03
<313> (1)..(745)

<400> 30

Met Ser Leu Lys Pro Arg Val Val Asp Phe Asp Glu Thr Trp Asn Lys
1 5 10 15

Leu Leu Thr Thr Ile Lys Ala Val Val Met Leu Glu Tyr Val Glu Arg
20 25 30

Ala Thr Trp Asn Asp Arg Phe Ser Asp Ile Tyr Ala Leu Cys Val Ala
35 40 45

Tyr Pro Glu Pro Leu Gly Glu Arg Leu Tyr Thr Glu Thr Lys Ile Phe
50 55 60

Leu Glu Asn His Val Arg His Leu His Lys Arg Val Leu Glu Ser Glu
65 70 75 80

Glu Gln Val Leu Val Met Tyr His Arg Tyr Trp Glu Glu Tyr Ser Lys
85 90 95

Gly Ala Asp Tyr Met Asp Cys Leu Tyr Arg Tyr Leu Ser Thr Gln Phe
 100 105 110

Ile Lys Lys Asn Lys Leu Thr Glu Ala Asp Leu Gln Tyr Gly Tyr Gly
 115 120 125

Gly Val Asp Met Asn Glu Pro Leu Met Glu Ile Gly Glu Leu Ala Leu
 130 135 140

Asp Met Trp Arg Lys Leu Met Val Glu Pro Leu Gln Ala Ile Leu Ile
 145 150 155 160

Arg Met Leu Leu Arg Glu Ile Lys Asn Asp Arg Gly Gly Glu Asp Pro
 165 170 175

Asn Gln Lys Val Ile His Gly Val Ile Asn Ser Phe Val His Val Glu
 180 185 190

Gln Tyr Lys Lys Lys Phe Pro Leu Lys Phe Tyr Gln Glu Ile Phe Glu
 195 200 205

Ser Pro Phe Leu Thr Glu Thr Gly Glu Tyr Tyr Lys Gln Glu Ala Ser
 210 215 220

Asn Leu Leu Gln Glu Ser Asn Cys Ser Gln Tyr Met Glu Lys Val Leu
 225 230 235 240

Gly Arg Leu Lys Asp Glu Glu Ile Arg Cys Arg Lys Tyr Leu His Pro
 245 250 255

Ser Ser Tyr Thr Lys Val Ile His Glu Cys Gln Gln Arg Met Val Ala
 260 265 270

Asp His Leu Gln Phe Leu His Ala Glu Cys His Asn Ile Ile Arg Gln
 275 280 285

Glu Lys Lys Asn Asp Met Ala Asn Met Tyr Val Leu Leu Arg Ala Val
 290 295 300

Ser Thr Gly Leu Pro His Met Ile Gln Glu Leu Gln Asn His Ile His
 305 310 315 320

Asp Glu Gly Leu Arg Ala Thr Ser Asn Leu Thr Gln Glu Asn Met Pro
 325 330 335

Thr Leu Phe Val Glu Ser Val Leu Glu Val His Gly Lys Phe Val Gln
340 345 350

Leu Ile Asn Thr Val Leu Asn Gly Asp Gln His Phe Met Ser Ala Leu
355 360 365

Asp Lys Ala Leu Thr Ser Val Val Asn Tyr Arg Glu Pro Lys Ser Val
370 375 380

Cys Lys Ala Pro Glu Leu Leu Ala Lys Tyr Cys Asp Asn Leu Leu Lys
385 390 395 400

Lys Ser Ala Lys Gly Met Thr Glu Asn Glu Val Glu Asp Arg Leu Thr
405 410 415

Ser Phe Ile Thr Val Phe Lys Tyr Ile Asp Asp Lys Asp Val Phe Gln
420 425 430

Lys Phe Tyr Ala Arg Met Leu Ala Lys Arg Leu Ile His Gly Leu Ser
435 440 445

Met Ser Met Asp Ser Glu Glu Ala Met Ile Asn Lys Leu Lys Gln Ala
450 455 460

Cys Gly Tyr Glu Phe Thr Ser Lys Leu His Arg Met Tyr Thr Asp Met
465 470 475 480

Ser Val Ser Ala Asp Leu Asn Asn Lys Phe Asn Asn Phe Ile Lys Asn
485 490 495

Gln Asp Thr Val Ile Asp Leu Gly Ile Ser Phe Gln Ile Tyr Val Leu
500 505 510

Gln Ala Gly Ala Trp Pro Leu Thr Gln Ala Pro Ser Ser Thr Phe Ala
515 520 525

Ile Pro Gln Glu Leu Glu Lys Ser Val Gln Met Phe Glu Leu Phe Tyr
530 535 540

Ser Gln His Phe Ser Gly Arg Lys Leu Thr Trp Leu His Tyr Leu Cys
545 550 555 560

Thr Gly Glu Val Lys Met Asn Tyr Leu Gly Lys Pro Tyr Val Ala Met
565 570 575

Val Thr Thr Tyr Gln Met Ala Val Leu Leu Ala Phe Asn Asn Ser Glu
580 585 590

Thr Val Ser Tyr Lys Glu Leu Gln Asp Ser Thr Gln Met Asn Glu Lys
595 600 605

Glu Leu Thr Lys Thr Ile Lys Ser Leu Leu Asp Val Lys Met Ile Asn
610 615 620

His Asp Ser Glu Lys Glu Asp Ile Asp Ala Glu Ser Ser Phe Ser Leu
625 630 635 640

Asn Met Asn Phe Ser Ser Lys Arg Thr Lys Phe Lys Ile Thr Thr Ser
645 650 655

Met Gln Lys Asp Thr Pro Gln Glu Met Glu Gln Thr Arg Ser Ala Val
660 665 670

Asp Glu Asp Arg Lys Met Tyr Leu Gln Ala Ala Ile Val Arg Ile Met
675 680 685

Lys Ala Arg Lys Val Leu Arg His Asn Ala Leu Ile Gln Glu Val Ile
690 695 700

Ser Gln Ser Arg Ala Arg Phe Asn Pro Ser Ile Ser Met Ile Lys Lys
705 710 715 720

Cys Ile Glu Val Leu Ile Asp Lys Gln Tyr Ile Glu Arg Ser Gln Ala
725 730 735

Ser Ala Asp Glu Tyr Ser Tyr Val Ala
740 745

<210> 31

<211> 768

<212> PRT

<213> Homo sapiens

<400> 31

Met Ser Asn Leu Ser Lys Gly Thr Gly Ser Arg Lys Asp Thr Lys Met
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Arg Ile Arg Ala Phe Pro Met Thr Met Asp Glu Lys Tyr Val Asn Ser
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Ile Trp Asp Leu Leu Lys Asn Ala Ile Gln Glu Ile Gln Arg Lys Asn
 35 40 45
 Asn Ser Gly Leu Ser Phe Glu Glu Leu Tyr Arg Asn Ala Tyr Thr Met
 50 55 60
 Val Leu His Lys His Gly Glu Lys Leu Tyr Thr Gly Leu Arg Glu Val
 65 70 75 80
 Val Thr Glu His Leu Ile Asn Lys Val Arg Glu Asp Val Leu Asn Ser
 85 90 95
 Leu Asn Asn Asn Phe Leu Gln Thr Leu Asn Gln Ala Trp Asn Asp His
 100 105 110
 Gln Thr Ala Met Val Met Ile Arg Asp Ile Leu Met Tyr Met Asp Arg
 115 120 125
 Val Tyr Val Gln Gln Asn Asn Val Glu Asn Val Tyr Asn Leu Gly Leu
 130 135 140
 Ile Ile Phe Arg Asp Gln Val Val Arg Tyr Gly Cys Ile Arg Asp His
 145 150 155 160
 Leu Arg Gln Thr Leu Leu Asp Met Ile Ala Arg Glu Arg Lys Gly Glu
 165 170 175
 Val Val Asp Arg Gly Ala Ile Arg Asn Ala Cys Gln Met Leu Met Ile
 180 185 190
 Leu Gly Leu Glu Gly Arg Ser Val Tyr Glu Glu Asp Phe Glu Ala Pro
 195 200 205
 Phe Leu Glu Met Ser Ala Glu Phe Phe Gln Met Glu Ser Gln Lys Phe
 210 215 220
 Leu Ala Glu Asn Ser Ala Ser Val Tyr Ile Lys Lys Val Glu Ala Arg
 225 230 235 240
 Ile Asn Glu Glu Ile Glu Arg Val Met His Cys Leu Asp Lys Ser Thr
 245 250 255
 Glu Glu Pro Ile Val Lys Val Val Glu Arg Glu Leu Ile Ser Lys His
 260 265 270

Met Lys Thr Ile Val Glu Met Glu Asn Ser Gly Leu Val His Met Leu
 275 280 285

Lys Asn Gly Lys Thr Glu Asp Leu Gly Cys Met Tyr Lys Leu Phe Ser
 290 295 300

Arg Val Pro Asn Gly Leu Lys Thr Met Cys Glu Cys Met Ser Ser Tyr
 305 310 315 320

Leu Arg Glu Gln Gly Lys Ala Leu Val Ser Glu Glu Gly Glu Gly Lys
 325 330 335

Asn Pro Val Asp Tyr Ile Gln Gly Leu Leu Asp Leu Lys Ser Arg Phe
 340 345 350

Asp Arg Phe Leu Leu Glu Ser Phe Asn Asn Asp Arg Leu Phe Lys Gln
 355 360 365

Thr Ile Ala Gly Asp Phe Glu Tyr Phe Leu Asn Leu Asn Ser Arg Ser
 370 375 380

Pro Glu Tyr Leu Ser Leu Phe Ile Asp Asp Lys Leu Lys Lys Gly Val
 385 390 395 400

Lys Gly Leu Thr Glu Gln Glu Val Glu Thr Ile Leu Asp Lys Ala Met
 405 410 415

Val Leu Phe Arg Phe Met Gln Glu Lys Asp Val Phe Glu Arg Tyr Tyr
 420 425 430

Lys Gln His Leu Ala Arg Arg Leu Leu Thr Asn Lys Ser Val Ser Asp
 435 440 445

Asp Ser Glu Lys Asn Met Ile Ser Lys Leu Lys Thr Glu Cys Gly Cys
 450 455 460

Gln Phe Thr Ser Lys Leu Glu Gly Met Phe Arg Asp Met Ser Ile Ser
 465 470 475 480

Asn Thr Thr Met Asp Glu Phe Arg Gln His Leu Gln Ala Thr Gly Val
 485 490 495

Ser Leu Gly Gly Val Asp Leu Thr Val Arg Val Leu Thr Thr Gly Tyr
 500 505 510

Trp Pro Thr Gln Ser Ala Thr Pro Lys Cys Asn Ile Pro Pro Ala Pro
515 520 525

Arg His Ala Phe Glu Ile Phe Arg Arg Phe Tyr Leu Ala Lys His Ser
530 535 540

Gly Arg Gln Leu Thr Leu Gln His His Met Gly Ser Ala Asp Leu Asn
545 550 555 560

Ala Thr Phe Tyr Gly Pro Val Lys Lys Glu Asp Gly Ser Glu Val Gly
565 570 575

Val Gly Gly Ala Gln Val Thr Gly Ser Asn Thr Arg Lys His Ile Leu
580 585 590

Gln Val Ser Thr Phe Gln Met Thr Ile Leu Met Leu Phe Asn Asn Arg
595 600 605

Glu Lys Tyr Thr Phe Glu Glu Ile Gln Gln Glu Thr Asp Ile Pro Glu
610 615 620

Arg Glu Leu Val Arg Ala Leu Gln Ser Leu Ala Cys Gly Lys Pro Thr
625 630 635 640

Gln Arg Val Leu Thr Lys Glu Pro Lys Ser Lys Glu Ile Glu Asn Gly
645 650 655

His Ile Phe Thr Val Asn Asp Gln Phe Thr Ser Lys Leu His Arg Val
660 665 670

Lys Ile Gln Thr Val Ala Ala Lys Gln Gly Glu Ser Asp Pro Glu Arg
675 680 685

Lys Glu Thr Arg Gln Lys Val Asp Asp Asp Arg Lys His Glu Ile Glu
690 695 700

Ala Ala Ile Val Arg Ile Met Lys Ser Arg Lys Lys Met Gln His Asn
705 710 715 720

Val Leu Val Ala Glu Val Thr Gln Gln Leu Lys Ala Arg Phe Leu Pro
725 730 735

Ser Pro Val Val Ile Lys Lys Arg Ile Glu Gly Leu Ile Glu Arg Glu
740 745 750

Tyr Leu Ala Arg Thr Pro Glu Asp Arg Lys Val Tyr Thr Tyr Val Ala
755 760 765

<210> 32
<211> 745
<212> PRT
<213> Homo sapiens

<300>
<308> Genbank/ AAD23581
<309> 1999-04-06
<313> (1)..(745)

<400> 32

Met Ser Leu Lys Pro Arg Val Val Asp Phe Asp Glu Thr Trp Asn Lys
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Leu Leu Thr Thr Ile Lys Ala Val Val Met Leu Glu Tyr Val Glu Arg
20 25 30

Ala Thr Trp Asn Asp Arg Phe Ser Asp Ile Tyr Ala Leu Cys Val Ala
35 40 45

Tyr Pro Glu Pro Leu Gly Glu Arg Leu Tyr Thr Glu Thr Lys Ile Phe
50 55 60

Leu Glu Asn His Val Arg His Leu His Lys Arg Val Leu Glu Ser Glu
65 70 75 80

Glu Gln Val Leu Val Met Tyr His Arg Tyr Trp Glu Glu Tyr Ser Lys
85 90 95

Gly Ala Asp Tyr Met Asp Cys Leu Tyr Arg Tyr Leu Asn Thr Gln Phe
100 105 110

Ile Lys Lys Asn Lys Leu Thr Glu Ala Asp Leu Gln Tyr Gly Tyr Gly
115 120 125

Gly Val Asp Met Asn Glu Pro Leu Met Glu Ile Gly Glu Leu Ala Leu
130 135 140

Asp Met Trp Arg Lys Leu Met Val Glu Pro Leu Gln Ala Ile Leu Ile
145 150 155 160

Arg Met Leu Leu Arg Glu Ile Lys Asn Asp Arg Gly Gly Glu Asp Pro
165 170 175

Asn Gln Lys Val Ile His Gly Val Ile Asn Ser Phe Val His Val Glu
 180 185 190

Gln Tyr Lys Lys Lys Phe Pro Leu Lys Phe Tyr Gln Glu Ile Phe Glu
 195 200 205

Ser Pro Phe Leu Thr Glu Thr Gly Glu Tyr Tyr Lys Gln Glu Ala Ser
 210 215 220

Asn Leu Leu Gln Glu Ser Asn Cys Ser Gln Tyr Met Glu Lys Val Leu
 225 230 235 240

Gly Arg Leu Lys Asp Glu Glu Ile Arg Cys Arg Lys Tyr Leu His Pro
 245 250 255

Ser Ser Tyr Thr Lys Val Ile His Glu Cys Gln Gln Arg Met Val Ala
 260 265 270

Asp His Leu Gln Phe Leu His Ala Glu Cys His Asn Ile Ile Arg Gln
 275 280 285

Glu Lys Lys Asn Asp Met Ala Asn Met Tyr Val Leu Leu Arg Ala Val
 290 295 300

Ser Thr Gly Leu Pro His Met Ile Gln Glu Leu Gln Asn His Ile His
 305 310 315 320

Asp Glu Gly Leu Arg Ala Thr Ser Asn Leu Thr Gln Glu Asn Met Pro
 325 330 335

Thr Leu Phe Val Glu Ser Val Leu Glu Val His Gly Lys Phe Val Gln
 340 345 350

Leu Ile Asn Thr Val Leu Asn Gly Asp Gln His Phe Met Ser Ala Leu
 355 360 365

Asp Lys Ala Leu Thr Ser Val Val Asn Tyr Arg Glu Pro Lys Ser Val
 370 375 380

Cys Lys Ala Pro Glu Leu Leu Ala Lys Tyr Cys Asp Asn Leu Leu Lys
 385 390 395 400

Lys Ser Ala Lys Gly Met Thr Glu Asn Glu Val Glu Asp Arg Leu Thr
 405 410 415

Ser Phe Ile Thr Val Phe Lys Tyr Ile Asp Asp Lys Asp Val Phe Gln
420 425 430

Lys Phe Tyr Ala Arg Met Leu Ala Lys Arg Leu Ile His Gly Leu Ser
435 440 445

Met Ser Met Asp Ser Glu Glu Ala Met Ile Asn Lys Leu Lys Gln Ala
450 455 460

Cys Gly Tyr Glu Phe Thr Ser Lys Leu His Arg Met Tyr Thr Asp Met
465 470 475 480

Ser Val Ser Ala Asp Leu Asn Asn Lys Phe Asn Asn Phe Ile Lys Asn
485 490 495

Gln Asp Thr Val Ile Asp Leu Gly Ile Ser Phe Gln Ile Tyr Val Leu
500 505 510

Gln Ala Gly Ala Trp Pro Leu Thr Gln Ala Pro Ser Ser Thr Phe Ala
515 520 525

Ile Pro Gln Glu Leu Glu Lys Ser Val Gln Met Phe Glu Leu Phe Tyr
530 535 540

Ser Gln His Phe Ser Gly Arg Lys Leu Thr Trp Leu His Tyr Leu Cys
545 550 555 560

Thr Gly Glu Val Lys Met Asn Tyr Leu Gly Lys Pro Tyr Val Ala Met
565 570 575

Val Thr Thr Tyr Gln Met Ala Val Leu Leu Ala Phe Asn Asn Ser Glu
580 585 590

Thr Val Ser Tyr Lys Glu Leu Gln Asp Ser Thr Gln Met Asn Glu Lys
595 600 605

Glu Leu Thr Lys Thr Ile Lys Ser Leu Leu Asp Val Lys Met Ile Asn
610 615 620

His Asp Ser Glu Lys Glu Asp Ile Asp Ala Glu Ser Ser Phe Ser Leu
625 630 635 640

Asn Met Asn Phe Ser Ser Lys Arg Thr Lys Phe Lys Ile Thr Thr Ser
645 650 655

Met Gln Lys Asp Thr Pro Gln Glu Met Glu Gln Thr Arg Ser Ala Val
660 665 670

Asp Glu Asp Arg Lys Met Tyr Leu Gln Ala Ala Ile Val Arg Ile Met
675 680 685

Lys Ala Arg Lys Val Leu Arg His Asn Ala Leu Ile Gln Glu Val Ile
690 695 700

Ser Gln Ser Arg Ala Arg Phe Asn Pro Ser Ile Ser Met Ile Lys Lys
705 710 715 720

Cys Ile Glu Val Leu Ile Asp Lys Gln Tyr Ile Glu Arg Ser Gln Ala
725 730 735

Ser Ala Asp Glu Tyr Ser Tyr Val Ala
740 745

<210> 33
<211> 770
<212> PRT
<213> Caenorhabditis elegans

<400> 33

Cys Asp Ser Glu Val Val Trp Lys Lys Leu Gln Asp Gly Leu Asp Val
1 5 10 15

Ala Tyr Arg Arg Glu Asn Met Ala Pro Lys Asp Tyr Met Thr Leu Tyr
20 25 30

Thr Ser Val Tyr Asp Tyr Cys Thr Ser Ile Thr Leu Ser Thr Ser Arg
35 40 45

Arg Asp Gly Glu Asp Gly Arg Ala Glu Ser Ser Thr Pro Ala Arg Thr
50 55 60

Ala Gly Ala Asp Phe Val Gly His Glu Met Tyr Gln Arg Val Glu Glu
65 70 75 80

Tyr Val Lys Ala Tyr Val Ile Ala Val Cys Glu Lys Gly Ala Glu Leu
85 90 95

Ser Gly Glu Asp Leu Leu Lys Tyr Tyr Thr Thr Glu Trp Glu Asn Phe
100 105 110

Arg Ile Ser Ser Lys Val Met Asp Gly Ile Phe Ala Tyr Leu Asn Arg
65

115					120					125					
His	Trp	Ile	Arg	Arg	Glu	Leu	Asp	Glu	Gly	His	Glu	Asn	Ile	Tyr	Met
130						135				140					
Val	Tyr	Thr	Leu	Ala	Leu	Val	Val	Trp	Lys	Arg	Asn	Leu	Phe	Asn	Asp
145					150					155					160
Leu	Lys	Asp	Lys	Val	Ile	Asp	Ala	Met	Leu	Glu	Leu	Ile	Arg	Ser	Glu
				165					170					175	
Arg	Thr	Gly	Ser	Met	Ile	Asn	Ser	Arg	Tyr	Ile	Ser	Gly	Val	Val	Glu
			180					185					190		
Cys	Leu	Val	Glu	Leu	Gly	Val	Asp	Asp	Ser	Glu	Thr	Asp	Ala	Lys	Lys
		195					200					205			
Asp	Ala	Glu	Thr	Lys	Lys	Leu	Ala	Val	Tyr	Lys	Glu	Phe	Phe	Glu	Val
	210					215					220				
Lys	Phe	Leu	Glu	Ala	Thr	Arg	Gly	Phe	Tyr	Thr	Gln	Glu	Ala	Ala	Asn
225					230					235					240
Phe	Leu	Ser	Asn	Gly	Gly	Asn	Val	Thr	Asp	Tyr	Met	Ile	Lys	Val	Glu
				245					250					255	
Thr	Arg	Leu	Asn	Gln	Glu	Asp	Asp	Arg	Cys	Gln	Leu	Tyr	Leu	Asn	Ser
			260					265					270		
Ser	Thr	Lys	Thr	Pro	Leu	Ala	Thr	Cys	Cys	Glu	Ser	Val	Leu	Ile	Ser
		275					280					285			
Asn	Gln	Leu	Asp	Phe	Leu	Gln	Arg	His	Phe	Gly	Gly	Leu	Leu	Val	Asp
		290				295					300				
Lys	Arg	Asp	Asp	Asp	Leu	Ser	Arg	Met	Phe	Lys	Leu	Cys	Asp	Arg	Val
305					310					315					320
Pro	Asn	Gly	Leu	Asp	Glu	Leu	Arg	Lys	Ser	Leu	Glu	Asn	His	Ile	Ala
				325					330					335	
Lys	Glu	Gly	His	Gln	Ala	Leu	Glu	Arg	Val	Ala	Met	Glu	Ala	Ala	Thr
			340					345					350		
Asp	Ala	Lys	Leu	Tyr	Val	Lys	Thr	Leu	Leu	Glu	Val	His	Glu	Arg	Tyr

355		360		365
Gln Ser Leu Val Asn Arg Ser Phe Lys Asn Glu Pro Gly Phe Met Gln				
370		375		380
Ser Leu Asp Lys Ala Ala Thr Ser Phe Ile Asn Asn Asn Ala Val Thr				
385		390		400
Lys Arg Ala Pro Pro Gln Ala Gln Leu Thr Lys Ser Ala Glu Leu Leu				
	405		410	415
Ala Arg Tyr Cys Asp Gln Leu Leu Arg Lys Ser Ser Lys Met Pro Asp				
	420		425	430
Glu Ala Glu Leu Glu Glu Leu Gln Thr Lys Ile Met Val Val Phe Lys				
	435		440	445
Tyr Ile Asp Asp Lys Asp Val Phe Ser Lys Phe Tyr Thr Lys Met Phe				
450		455		460
Ser Lys Arg Leu Ile Ser Glu Leu Ser Ala Ser Asp Glu Ala Glu Ala				
465		470		475
Asn Phe Ile Thr Lys Leu Lys Ser Met Cys Gly Tyr Glu Tyr Thr Ala				
	485		490	495
Arg Leu Ser Lys Met Val Asn Asp Thr Gln Val Ser Lys Asp Leu Thr				
	500		505	510
Ala Asp Phe Lys Glu Lys Lys Ala Asp Met Leu Gly Gln Lys Ser Val				
	515		520	525
Glu Phe Asn Val Leu Val Leu Ser Ser Gly Ser Trp Pro Thr Phe Pro				
530		535		540
Thr Thr Pro Ile Thr Leu Pro Gln Gln Leu Ser Lys Thr Ile Glu Ile				
545		550		555
Phe Gly Gln Phe Tyr Asn Glu Lys Phe Asn Gly Arg Arg Leu Thr Trp				
	565		570	575
Val Tyr Ser Gln Ser Arg Gly Glu Ile Thr Ser Thr Ala Phe Pro Lys				
	580		585	590
Lys Tyr Val Phe Thr Ala Thr Thr Ala Gln Met Cys Thr Met Leu Leu				

595	600	605
Phe Asn Glu Gln Asp Ser Tyr Thr Val Glu Gln Ile Ala Ala Ala Thr		
610	615	620
Lys Met Asp Glu Lys Ser Ala Pro Ala Ile Val Gly Ser Leu Ile Lys		
625	630	635 640
Asn Leu Val Leu Lys Ala Asp Thr Glu Leu Gln Lys Glu Asp Glu Val		
	645	650 655
Pro Met Thr Ala Thr Val Ser Leu Asn Lys Ala Tyr Met Asn Lys Lys		
	660	665 670
Val Arg Val Asp Leu Ser Lys Phe Thr Met Lys Gln Asp Ala Val Arg		
	675	680 685
Asp Thr Glu Asn Val Gln Lys Asn Val Glu Glu Asp Arg Lys Ser Val		
	690	695 700
Ile Ser Ala Cys Ile Val Arg Ile Met Lys Thr Arg Lys Arg Val Gln		
705	710	715 720
His Gln Gln Leu Met Thr Glu Val Ile Thr Gln Leu Ser Gly Arg Phe		
	725	730 735
Lys Pro Lys Val Glu Met Ile Lys Arg Cys Ile Gly Ser Leu Ile Glu		
	740	745 750
Lys Glu Tyr Met Leu Arg Thr Glu Gly Gln Lys Asp Leu Tyr Glu Tyr		
	755	760 765
Leu Ala		
770		

<210> 34
 <211> 773
 <212> PRT
 <213> Drosophila melanogaster

<300>
 <308> Genbank/AAA85085
 <309> 1996-01-03
 <313> (1) .. (773)

<400> 34

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Asp	Asp	Ile	Trp
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Ser	Glu	Leu	Val
		25	
Glu	Gly	Ile	Met
Gln	Val	Phe	Glu
	30		
His	Glu	Lys	Ser
	35		
Leu	Thr	Arg	Ser
		40	
Gln	Tyr	Met	Arg
Phe	Tyr	Thr	His
	45		
Val	Tyr	Asp	Tyr
	50		
Cys	Thr	Ser	Val
		55	
Ser	Ala	Ala	Pro
			60
Ser	Gly	Arg	Ser
Ser	Gly	Lys	Thr
	65		
Gly	Gly	Ala	Gln
	70		
Leu	Val	Gly	Lys
		75	
Lys	Lys	Leu	Tyr
			80
Arg	Leu	Glu	Gln
Phe	Leu	Lys	Ser
	85		
Tyr	Leu	Ser	Glu
		90	
Leu	Leu	Thr	Lys
			95
Phe	Lys	Ala	Ile
Ser	Gly	Glu	Glu
	100		
Val	Leu	Leu	Ser
		105	
Arg	Tyr	Thr	Lys
			110
Gln	Trp	Lys	Ser
	115		
Tyr	Gln	Phe	Ser
Ser	Ser	Thr	Val
	120		
Leu	Asp	Gly	Ile
		125	
Cys			
Asn	Tyr	Leu	Asn
	130		
Arg	Asn	Trp	Val
		135	
Lys	Arg	Glu	Cys
			140
Glu	Glu	Gly	Gln
Lys	Gly	Ile	Tyr
	145		
Lys	Ile	Tyr	Arg
		150	
Leu	Ala	Leu	Val
		155	
Ala	Trp	Lys	Gly
			160
His	Leu	Phe	Gln
Val	Leu	Asn	Glu
	165		
Pro	Val	Thr	Lys
		170	
Ala	Val	Leu	Lys
			175
Ser	Ile	Glu	Glu
Glu	Arg	Gln	Gly
	180		
Lys	Leu	Ile	Asn
Arg	Ser	Leu	Val
		185	
Val	Glu	Leu	Ser
Phe	Asn	Glu	Glu
		190	
Asp			
Arg	Asp	Val	Ile
	195		
Glu	Cys	Tyr	Val
Glu	Leu	Ser	Phe
		200	
Asn	Glu	Glu	Asp
			205
Thr	Asp	Ala	Glu
	210		
Gln	Gln	Lys	Leu
Ser	Val	Tyr	Lys
			215
Gln	Asn	Phe	Glu
			220
Asn	Lys	Phe	Ile
	225		
Ala	Asp	Thr	Ser
		230	
Ala	Phe	Tyr	Glu
		235	
Lys	Glu	Ser	Asp
			240
Ala	Phe	Leu	Ser
Thr	Asn	Thr	Val
Thr	Glu	Tyr	Leu
Lys	His	Val	Glu

245										250					255				
Asn	Arg	Leu	Glu	Glu	Glu	Thr	Gln	Arg	Arg	Gly	Phe	Asn	Ser	Lys	Asn				
			260					265					270						
Gly	Leu	Ser	Tyr	Leu	His	Glu	Thr	Thr	Ala	Asp	Val	Leu	Lys	Ser	Thr				
		275					280					285							
Cys	Glu	Glu	Val	Leu	Ile	Glu	Lys	His	Leu	Lys	Ile	Phe	His	Thr	Glu				
	290					295					300								
Phe	Gln	Asn	Leu	Leu	Asn	Ala	Asp	Arg	Asn	Asp	Asp	Leu	Lys	Arg	Met				
305					310					315					320				
Tyr	Ser	Leu	Val	Ala	Leu	Ser	Ser	Lys	Asn	Leu	Thr	Asp	Leu	Lys	Ser				
				325					330					335					
Ile	Leu	Glu	Asn	His	Ile	Leu	His	Gln	Gly	Thr	Glu	Ala	Ile	Ala	Lys				
			340					345					350						
Cys	Cys	Thr	Thr	Asp	Ala	Ala	Asn	Asp	Pro	Lys	Thr	Tyr	Val	Gln	Thr				
		355					360					365							
Ile	Leu	Asp	Val	His	Lys	Lys	Tyr	Asn	Ala	Leu	Val	Leu	Thr	Ala	Phe				
	370					375					380								
Asn	Asn	Asp	Asn	Gly	Phe	Val	Ala	Ala	Leu	Asp	Lys	Ala	Cys	Gly	Lys				
385					390					395					400				
Phe	Ile	Asn	Ser	Asn	Val	Val	Thr	Ile	Ala	Asn	Ser	Ala	Ser	Lys	Ser				
				405					410					415					
Pro	Glu	Leu	Leu	Ala	Lys	Tyr	Cys	Asp	Leu	Leu	Leu	Lys	Lys	Ser	Ser				
			420					425					430						
Lys	Asn	Pro	Glu	Asp	Lys	Glu	Leu	Glu	Asp	Asn	Leu	Asn	Gln	Val	Met				
		435					440					445							
Val	Val	Phe	Lys	Tyr	Ile	Glu	Asp	Lys	Asp	Val	Phe	Gln	Lys	Tyr	Tyr				
	450					455					460								
Ser	Lys	Met	Leu	Ala	Lys	Arg	Leu	Val	Asn	His	Thr	Ser	Ala	Ser	Asp				
465					470					475					480				
Asp	Ala	Glu	Ala	Met	Met	Ile	Ser	Lys	Leu	Lys	Gln	Thr	Cys	Gly	Tyr				

485								490					495				
Glu	Tyr	Thr	Val	Lys	Leu	Gln	Arg	Met	Phe	Gln	Asp	Ile	Gly	Val	Ser		
			500					505					510				
Lys	Asp	Leu	Asn	Ser	Tyr	Phe	Lys	Gln	Tyr	Leu	Ala	Glu	Lys	Asn	Leu		
		515					520					525					
Thr	Met	Glu	Ile	Asp	Phe	Gly	Ile	Glu	Val	Leu	Ser	Ser	Gly	Ser	Trp		
	530					535					540						
Pro	Phe	Gln	Leu	Ser	Asn	Asn	Phe	Leu	Leu	Pro	Ser	Glu	Leu	Glu	Arg		
545					550					555					560		
Ser	Val	Arg	Gln	Phe	Asn	Glu	Phe	Tyr	Ala	Ala	Arg	His	Ser	Gly	Arg		
				565					570					575			
Lys	Leu	Asn	Trp	Leu	Tyr	Gln	Met	Cys	Lys	Gly	Glu	Leu	Ile	Met	Asn		
			580					585					590				
Val	Asn	Arg	Asn	Asn	Ser	Ser	Thr	Tyr	Thr	Leu	Gln	Ala	Ser	Thr	Phe		
		595					600					605					
Gln	Met	Ser	Val	Leu	Leu	Gln	Phe	Asn	Asp	Gln	Leu	Ser	Phe	Thr	Val		
	610					615					620						
Gln	Gln	Leu	Gln	Asp	Asn	Thr	Gln	Thr	Gln	Gln	Glu	Asn	Leu	Ile	Gln		
625					630					635					640		
Val	Leu	Gln	Ile	Leu	Leu	Lys	Ala	Lys	Val	Leu	Thr	Ser	Ser	Asp	Asn		
				645					650					655			
Glu	Asn	Ser	Leu	Thr	Pro	Glu	Ser	Thr	Val	Glu	Leu	Phe	Leu	Asp	Tyr		
			660					665					670				
Lys	Asn	Lys	Lys	Arg	Arg	Ile	Asn	Ile	Asn	Gln	Pro	Leu	Lys	Thr	Glu		
		675					680					685					
Leu	Lys	Val	Glu	Gln	Glu	Thr	Val	His	Lys	His	Ile	Glu	Glu	Asp	Arg		
	690					695					700						
Lys	Leu	Leu	Ile	Gln	Ala	Ala	Ile	Val	Arg	Ile	Met	Lys	Met	Arg	Lys		
705					710					715					720		
Arg	Leu	Asn	His	Thr	Asn	Leu	Ile	Ser	Glu	Val	Leu	Asn	Gln	Leu	Ser		

725

730

735

Thr Arg Phe Lys Pro Lys Val Pro Val Ile Lys Lys Cys Ile Asp Ile
 740 745 750

Leu Ile Glu Lys Glu Tyr Leu Glu Arg Met Glu Gly His Lys Asp Thr
 755 760 765

Tyr Ser Tyr Leu Ala
 770

<210> 35
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 <212> PRT
 <213> Schizosaccharomyces pombe

<300>
 <308> Q10452
 <309> 2003-09-15
 <313> (1)..(387)

<400> 35

Met Asn His Gly Thr Lys Ile Pro Val Asp Pro Phe Arg Ile Ile Lys
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Glu Thr Ala Arg Asp Gly Ser Thr Gly Glu Val Lys Gln Leu Ser Tyr
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Thr Ser Ser Lys Val Val Gly Ser Gly Ser Phe Gly Val Val Met Gln
 35 40 45

Val His Leu Ile Glu Ser Asp Ser Lys Ala Ala Ile Lys Arg Val Leu
 50 55 60

Gln Asp Lys Arg Phe Lys Asn Arg Glu Leu Gln Ile Met Arg Ile Met
 65 70 75 80

Lys His Pro Asn Ile Val Asp Leu Ile Ala Tyr Tyr Tyr Thr Thr Gly
 85 90 95

Asp Asn Ser Asp Glu Val Tyr Leu Asn Leu Val Leu Glu Phe Met Pro
 100 105 110

Glu Thr Ile Tyr Arg Ala Ser Arg Leu Tyr Thr Arg Gln Lys Leu Ser
 115 120 125

Met Pro Met Leu Glu Val Lys Leu Tyr Ile Tyr Gln Leu Leu Arg Ser
 72

130		135		140
Leu Ala Tyr Ile His	Ala Ser Gly Ile Cys His	Arg Asp Ile Lys Pro		
145	150	155	160	
Gln Asn Leu Leu Leu	Asp Pro Glu Asn Gly Ile	Leu Lys Leu Cys Asp		
	165	170	175	
Phe Gly Ser Ala Lys	Ile Leu Val Ala Gly Glu	Pro Asn Val Ser Tyr		
	180	185	190	
Ile Cys Ser Arg Tyr	Tyr Arg Ala Pro Glu Leu	Ile Phe Gly Ala Thr		
	195	200	205	
Asp Tyr Thr His Ala	Ile Asp Ile Trp Ser Thr	Gly Cys Val Met Ala		
	210	215	220	
Glu Leu Met Leu Gly	His Pro Leu Phe Pro	Gly Glu Ser Gly Ile	Asp	
225	230	235	240	
Gln Leu Val Glu Ile	Ile Lys Ile Leu Gly Thr	Pro Ser Arg Glu Gln		
	245	250	255	
Ile Lys Thr Met Asn	Pro Asn Tyr Met Glu His	Arg Phe Pro Gln Ile		
	260	265	270	
Arg Pro Gln Pro Leu	Ser Arg Val Phe Ser Arg	Ser Val Pro Leu Asp		
	275	280	285	
Ala Leu Asp Leu Leu	Ser Lys Met Leu Gln Tyr	Thr Pro Thr Asp Arg		
	290	295	300	
Leu Thr Ala Ala Glu	Ala Met Cys His Pro Phe	Phe Asp Glu Leu Arg		
305	310	315	320	
Asp Pro Asn Thr Lys	Leu His Asn Ser Arg Asn	Pro Asp Ala Ser Pro		
	325	330	335	
Arg His Leu Pro Glu	Leu Phe Asn Phe Ser Pro	Phe Glu Leu Ser Ile		
	340	345	350	
Arg Pro Asp Leu Asn	Gln Lys Leu Ile Pro Ser	His Ala Arg Asp Ala		
	355	360	365	
Leu Pro Val Lys Leu	Asp Asp Phe Val Pro Ile	Pro Ile His Arg Ala		

370

375

380

Arg Ile Asp
385

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Met Ser Lys Ile Lys Leu Ile Ser Ser Asp Asn Glu Glu Phe Val Val
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Asp Gln Leu Ile Ala Glu Arg Ser Met Leu Ile Lys Asn Met Leu Glu
20 25 30

Asp Val Gly Glu Ile Asn Val Pro Ile Pro Leu Pro Asn Val Ser Ser
35 40 45

Asn Val Leu Arg Lys Val Leu Glu Trp Cys Glu His His Lys Asn Asp
50 55 60

Leu Tyr Ser Gly Thr Glu Glu Glu Ser Asp Ile Arg Leu Lys Lys Ser
65 70 75 80

Thr Asp Ile Asp Glu Trp Asp Arg Lys Phe Met Ala Val Asp Gln Glu
85 90 95

Met Leu Phe Glu Ile Val Leu Ala Ser Asn Tyr Leu Asp Ile Lys Pro
100 105 110

Leu Leu Asp Thr Gly Cys Lys Thr Val Ala Asn Met Ile Arg Gly Lys
115 120 125

Ser Pro Glu Asp Ile Arg Lys Thr Phe Asn Ile Pro Asn Asp Phe Thr
130 135 140

Pro Glu Glu Glu Glu Gln Ile Arg Lys Glu Asn Glu Trp Ala Glu Asp
145 150 155 160

Arg

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Met Val Thr Ser Asn Val Val Leu Val Ser Gly Glu Gly Glu Arg Phe
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Thr Val Asp Lys Lys Ile Ala Glu Arg Ser Leu Leu Leu Lys Asn Tyr
20 25 30

Leu Asn Asp Met His Asp Ser Asn Leu Gln Asn Asn Ser Asp Ser Asp
35 40 45

Ser Asp Ser Asp Ser Glu Thr Asn His Lys Ser Lys Asp Asn Asn Asn
50 55 60

Gly Asp Asp Asp Asp Glu Asp Asp Asp Glu Ile Val Met Pro Val Pro
65 70 75 80

Asn Val Arg Ser Ser Val Leu Gln Lys Val Ile Glu Trp Ala Glu His
85 90 95

His Arg Asp Ser Asn Phe Pro Asp Glu Asp Asp Asp Asp Ser Arg Lys
100 105 110

Ser Ala Pro Val Asp Ser Trp Asp Arg Glu Phe Leu Lys Val Asp Gln
115 120 125

Glu Met Leu Tyr Glu Ile Ile Leu Ala Ala Asn Tyr Leu Asn Ile Lys
130 135 140

Pro Leu Leu Asp Ala Gly Cys Lys Val Val Ala Glu Met Ile Arg Gly
145 150 155 160

Arg Ser Pro Glu Glu Ile Arg Arg Thr Phe Asn Ile Val Asn Asp Phe
165 170 175

Thr Pro Glu Glu Glu Ala Ala Ile Arg Arg Glu Asn Glu Trp Ala Glu
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180

185

190

Asp Arg

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Met Val Thr Ser Asn Val Val Leu Val Ser Gly Glu Gly Glu Arg Phe
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Thr Val Asp Lys Lys Ile Ala Glu Arg Ser Leu Leu Leu Lys Asn Tyr
 20 25 30

Leu Asn Asp Met His Asp Ser Asn Leu Gln Asn Asn Ser Asp Ser Glu
 35 40 45

Ser Asp Ser Asp Ser Glu Thr Asn His Lys Ser Lys Asp Asn Asn Asn
 50 55 60

Gly Asp Asp Asp Asp Glu Asp Asp Asp Glu Ile Val Met Pro Val Pro
 65 70 75 80

Asn Val Arg Ser Ser Val Leu Gln Lys Val Ile Glu Trp Ala Glu His
 85 90 95

His Arg Asp Ser Asn Phe Pro Asp Glu Asp Asp Asp Asp Ser Arg Lys
 100 105 110

Ser Ala Pro Val Asp Ser Trp Asp Arg Glu Phe Leu Lys Val Asp Gln
 115 120 125

Glu Met Leu Tyr Glu Ile Ile Leu Ala Ala Asn Tyr Leu Asn Ile Lys
 130 135 140

Pro Leu Leu Asp Ala Gly Cys Lys Val Val Ala Glu Met Ile Arg Gly
 145 150 155 160

Arg Ser Pro Glu Glu Ile Arg Arg Thr Phe Asn Ile Val Asn Asp Phe

165

170

175

Thr Pro Glu Glu Glu Ala Ala Ile Arg Arg Glu Asn Glu Trp Ala Glu
 180 185 190

Asp Arg

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Asp Ser Gly Xaa Xaa Ser
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Phe Leu Pro Thr Pro Val Leu Glu Asp
1 5